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(54) Title: MODULATING DEVELOPMENTAL PATHWAYS IN PLANTS

(57) Abstract: The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein.

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Title: Modulating developmental pathways in plants.

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The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The 10 different domains of RKS gene products essentially have the following functions: The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature 15 protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate 20 bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein 25 residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a single transmembrane domain. At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with 30 serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062, WO 01/29240). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

Plant homologs of the *Arabidopsis* RKS genes can be found by comparison of various plant database (see also Table 2) and comprise amongst others:

- 5 Y14600|SBRLK1|Sorghum bicolor
BF004020|BF004020|EST432518 KV1 Medicago truncatata
AW934655|AW934655|EST353547 tomato
AW617954|AW617954|EST314028 L. pennellii
AA738544|AA738544|SbRLK2 Sorghum bicolor
- 10 AA738545|AA738545|SbRLK3 Sorghum bicolor
BG595415|BG595415|EST494093 cSTS Solanum tuberosa
AI896277|AI896277|EST265720 tomato
BF643238|BF643238|NF002H05EC1F1045
AA738546|AA738546|SbRLK4 Sorghum bicolor
- 15 BE658174|BE658174|GM700005A20D5 Gm-r1070 Glycine max
BF520845|BF520845|EST458318 DSIL Medicago truncata
AC069324|AC069324|Oryza sativa
AW761055|AW761055|sl70d06.y1 Gm-c1027 Glycine max
BE352622|BE352622|WHE0425_G11_M21ZS Wheat
- 20 BG647340|BG647340|EST508959 HOGA Medicago truncata
AY028699|AY028699|Brassica napus
AW666082|AW666082|sk31h04.y1 Gm-c1028 Glycine max
AA738547|AA738547|SbRLK5 Sorghum bicolor
BG127658|BG127658|EST473220 tomato
- 25 L27821|RICPRKI|Oryza sativa
BG238468|BG238468|sab51a09.y1 Gm-c1043 Glycine max
BG441204|BG441204|GA_Ea0012C15f Gossypium arbo.
AW667985|AW667985|GA_Ea0012C15 Gossypium arbore.
AW233982|AW233982|sf32g05.y1 Gm-c1028 Glycine max
- 30 AP003235|AP003235|Oryza sativa
BF460294|BF460294|074A05 Mature tuber
AY007545|AY007545|Brassica napus
AC087544|AC087544|Oryza sativa
AB041503|AB041503|Populus nigra

35

The invention furthermore relates to modifying ELS genes or gene products or functional equivalents thereof which are for example derived from at least two different genes in the *Arabidopsis* genome. They show high homology on protein level

with the corresponding transmembrane RKS gene products.

However, they lack a transmembrane domain while they do contain a signaling sequence at the N-terminal end. Therefore these proteins are thought to be positioned within vesicles

5 within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologs have been detected in other plant species, such as:

AF370543|AF370543|*Arabidopsis thaliana*

10 AF324989|AF324989|*Arabidopsis thaliana*

AV520367|AV520367|*Arabidopsis thaliana*

AV553051|AV553051|*Arabidopsis thaliana*

BF642233|BF642233|NF050C09IN1F1069

AW559436|AW559436|EST314484 DSIR *Medicago truncata*

15 BG456991|BG456991|NF099F02PL1F1025

AW622146|AW622146|EST312944 tomato

BF260895|BF260895|HVSMEf0023D15f *Hordeum vulgare*

BE322325|BE322325|NF022E12IN1F1088

BG414774|BG414774|HVSMEk0003K21f *Hordeum vulgare*

20 BE460627|BE460627|EST412046 tomato

BI204894|BI204894|EST522934 cTOS *Lycopersicon esculentum*

BI205306|BI205306|EST523346 cTOS *Lycopersicon esculentum*

BI204366|BI204366|EST522406 cTOS *Lycopersicon esculentum*

AW443205|AW443205|EST308135 tomato

25 AW031110|AW031110|EST274417 tomato

BI180080|BI180080|EST521025 cSTE *Solanum tuberosa*

BF644761|BF644761|NF015A11EC1F1084

AV526127|AV526127|*Arabidopsis thaliana*

AV556193|AV556193|*Arabidopsis thaliana*

30 BE203316|BE203316|EST403338 KV1 *Medicago truncatata*.

AW649615|AW649615|EST328069 tomato

BE512465|BE512465|946071E06

BI204917|BI204917|EST522957 cTOS *Lycopersicon esculentum*

BG590749|BG590749|EST498591

35 BG648725|BG648725|EST510344 HOGA *Medicago truncata*

BG648619|BG648619|EST510238 HOGA *Medicago truncata*

BG597757|BG597757|EST496435 cSTS *Solanum tuberosa*

AW221939|AW221939|EST298750 tomato

BE704836|BE704836|Sc01_

40 BG124409|BG124409|EST470055 tomato

BF051954 | BF051954 | EST437120 tomato
BG320355 | BG320355 | Zm03_05h01_Zea mays
AV526624 | AV526624 | *Arabidopsis thaliana*
AW933960 | AW933960 | EST359803 tomato
5 AW221278 | AW221278 | EST297747 tomato
BE405514 | BE405514 | WHE1212_C01_F02ZS Wheat
BG314461 | BG314461 | WHE2495_A12_A23ZS *Triticum*
BF258673 | BF258673 | HVSMEf0016G01f *Hordeum vulgare*
BG262637 | BG262637 | WHE0938_E03_I06ZS Wheat
10 AW030188 | AW030188 | EST273443 tomato
BG653580 | BG653580 | sad76b11.y1 Gm-c1051 *Glycine max*
BG319729 | BG319729 | Zm03_05h01_A Zm03_Zea mays
BF053590 | BF053590 | EST438820 potato
BE454808 | BE454808 | HVSMEh0095C03f *Hordeum vulgare*
15 BI075801 | BI075801 | PI1_21_D05.b1_A002
BE367593 | BE367593 | PI1_9_F02.b1_A002 *Sorghum bicolor*
2e-074 BF260080 | BF260080 | HVSMEf0021A22f *Hordeum vulgare*
BF627921 | BF627921 | HVSMEb0006I23f *Hordeum vulgare*
BG598491 | BG598491 | EST503391 cSTS *Solanum tuberosa*
20 AW038168 | AW038168 | EST279825 tomato
BG343258 | BG343258 | HVSMEg0005D23f *Hordeum vulgare*
AW925684 | AW925684 | HVSMEg0005D23 *Hordeum vulgare*
BG416093 | BG416093 | HVSMEk0009L18f *Hordeum vulgare*
AW683370 | AW683370 | NF011C09LF1F1069
25 BE420108 | BE420108 | WWS020.C1R000101 ITEC WWS Wheat
AW350720 | AW350720 | GM210009A10F4 Gm-r1021 *Glycine max*
AW616564 | AW616564 | EST322975 L. *Hirsutum trichome*
AW011134 | AW011134 | ST17B03 Pine
BF630746 | BF630746 | HVSMEb0013N06f *Hordeum vulgare*
30 AW926045 | AW926045 | HVSMEg0006C10 *Hordeum vulgare*
BE519800 | BE519800 | HV_CEb0021E12f *Hordeum vulgare*
BG343657 | BG343657 | HVSMEg0006C10f *Hordeum vulgare*
BG933682 | BG933682 | OV1_16_C09.b1_A002
BE433368 | BE433368 | EST399897 tomato
35 AW219797 | AW219797 | EST302279 tomato
BF629324 | BF629324 | HVSMEb0010N06f *Hordeum vulgare*
BE597128 | BE597128 | PI1_71_A07.g1_A002
AW220075 | AW220075 | EST302558 tomato
AW616639 | AW616639 | EST323050 L. *Hirsutum trichome*
40 BF645214 | BF645214 | NF032F11EC1F1094
AW924540 | AW924540 | WS1_70_H12.b1_A002

AI775448|AI775448|EST256548 tomato

AW983360|AW983360|HVSMEg0010F15f *Hordeum vulgare*

BF270171|BF270171|GA_Eb0007B13f *Gossypium arbor.*

BE919631|BE919631|EST423400 potato

5 AW037836|AW037836|EST279465 tomato

BF008781|BF008781|ss79h09.y1 Gm-c1064 *Glycine max*

BF254651|BF254651|HVSMEf0004K05f *Hordeum vulgare*

BE599797|BE599797|PI1_79_H01.g1_A002

BE599026|BE599026|PI1_86_E03.g1_A002

10 R89998|R89998|16353 Lambda-PRL2 *Arabidopsis*

BG841108|BG841108|MEST15-G02.T3 ISUM4-TN *Zea mays*

AW307218|AW307218|sf54c07.y1 Gm-c1009 *Glycine max*

AI496325|AI496325|sb05c09.y1 Gm-c1004 *Glycine max*

AJ277703|ZMA277703|Zea mays

15 AL375586|CNS0616P|Medicago truncatula EST

AW350549|AW350549|GM210009A10A12 Gm-r1021 *Glycine max*

BE125918|BE125918|DG1_59_F02.b1_A002

BF053901|BF053901|EST439131 potato

BE921389|BE921389|EST425266 potato

20 BE597551|BE597551|PI1_71_A07.b1_

BE360092|BE360092|DG1_61_C09.b1_A002

BE660084|BE660084|491 GmaxSC *Glycine max*

AJ277702|ZMA277702|Zea mays

25 The invention also relates to modifying SBP/SPL gene or products which represent a family of transcription factors with a bipartite nuclear localization signal (The SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE (SBP/SPL) gene family of *Arabidopsis thaliana*, Columbia ecotype). Upon activation (probably by RKS mediated phosphorylation, the bipartite nuclear localization signal becomes linear and available for the nuclear translocation of the protein. Within the plant nucleus, the transcription factor regulates transcription by interaction with specific promoter elements. In *Arabidopsis thaliana*, this family is represented by at least 16 different members (see following list). In many other plant species, we also identified members of this transcription factor family (See list on page 7).

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Functional interaction between RKS and SBP proteins was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter (data not shown). At the tip of double overexpressing plants, embryo structures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signalling cascade, resulting in the reprogramming of developmental fate of a determined meristem. (ref. dissertation:
<http://www.ub.uni-koeln.de/ediss/archiv/2001/11w1204.pdf>;
Plant Journal 1997: 12, 2 367-377; Mol. Gen. Genet. 1996: 250, 7-16; Gene 1999, 237, 91-104, Genes and Development 1997: 11, 616-628), Proc. Natl. Acad. Sci. USA 1998: 95, 10306-10311; The Plant Journal 2000: 22, 523-529; Science 1997: 278, 1963-1965; Plant Physiol. Biochem. 2000: 38, 789-796; Cell 1996: 84, 61-71; Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

20

	name	genetic code
	ATSPL1	At2g47070*
	ATSPL2	At5g43270
	ATSPL3	At2g33810*
25	ATSPL4	At1g53160*
	ATSPL5	At3g15270
	ATSPL6	At1g69170
	ATSPL7	At5g18830
	ATSPL8	At1g02065
30	ATSPL9	At2g42200*
	ATSPL10	At1g27370*
	ATSPL11	At1g27360*
	ATSPL12	At3g60030
	ATSPL13	At5g50570
35	ATSPL14	At1g20980
	ATSPL15	At3g57920
	ATSPL16	At1g76580

* annotation in database not complete and/or correct

In many other plant species, we identified members of this transcription factor family, plant homologs of the Arabidopsis SBP/SPL proteins are for example:

- 5 AB023037 | AB023037 | *Arabidopsis thaliana*
 BG789832 | BG789832 | sae56b07.y1 Gm-cl051 *Glycine max*
 BG123992 | BG123992 | EST469638 *tomato*
 BG595750 | BG595750 | EST494428 cSTS *Solanum tuberosum*
 AF370612 | AF370612 | *Arabidopsis thaliana*
10 BF728335 | BF728335 | 1000060H02.x1 1000 - *Zea mays*
 X92079 | AMSBP2 | *A.majus*
 AW331087 | AW331087 | 707047A12.x1 707 - Mixed adult... 128 *zea mays*
 AJ011643 | ATH011643 | *Arabidopsis thaliana*
 L34039 | RICRMSOA | *Oryza sativa*
15 AJ011638 | ATH011638 | *Arabidopsis thaliana*
 AJ011639 | ATH011639 | *Arabidopsis thaliana*
 AJ132096 | ATH132096 | *Arabidopsis thaliana*
 BF482644 | BF482644 | WHE2301-2304_A21_A21ZS *Wheat*
 BF202242 | BF202242 | WHE0984_D01_G02ZS *Wheat*
20 BE057470 | BE057470 | sm58e10.y1 Gm-cl028 *Glycine max*
 AJ011628 | ATH011628 | *Arabidopsis thaliana*
 AJ011629 | ATH011629 | *Arabidopsis thaliana*
 AJ011617 | ZMA011617 | *Zea mays*
 AJ011637 | ATH011637 | *Arabidopsis thaliana*
25 AJ011622 | AMA011622 | *Antirrhinum majus*
 AJ011621 | AMA011621 | *Antirrhinum majus*
 AJ011635 | ATH011635 | *Arabidopsis thaliana*
 AJ011623 | AMA011623 | *Antirrhinum majus*
 BF650908 | BF650908 | NF098D09EC1F1076
30 AJ242959 | ATH242959 | *Arabidopsis thaliana*
 Y09427 | ATSPL3 | *A. thaliana* mRNA
 AJ011633 | ATH011633 | *Arabidopsis thaliana*
 AW691786 | AW691786 | NF044B06ST1F1000
 BE058432 | BE058432 | sn16a06.y1 Gm-cl016 *Glycine max*
35 AW728623 | AW728623 | GA_Ea0017G06 *Gossypium arbore.*
 BG442540 | BG442540 | GA_Ea0017G06f *Gossypium arbo.*
 AJ011626 | ATH011626 | *Arabidopsis thaliana*
 AJ011625 | ATH011625 | *Arabidopsis thaliana*
 AI993858 | AI993858 | 701515182 *A. thaliana*
40 BG593787 | BG593787 | EST492465 cSTS *Solanum tuberosum*
 BF634536 | BF634536 | NF060C08DT1F1065 *Drought Medicago*

BE806499|BE806499|ss59f10.y1 Gm-c1062 Glycine max
AW933950|AW933950|EST359793 tomato
AC008262|AC008262| Arabidopsis
B28493|B28493|T10A24TF TAMU Arabidopsis thaliana

5 AJ011644|ATH011644|Arabidopsis thaliana
AC018364|AC018364|Arabidopsis thaliana
AL092429|CNS00VLB|Arabidopsis thaliana
BE435668|BE435668|EST406746 tomato
BG097153|BG097153|EST461672 potato

10 BE440574|BE440574|sp47b09.y1 Gm-c1043 Glycine max
AI443033|AI443033|sa31a08.y1 Gm-c1004 Glycine max
U89496|ZMU89496|Zea mays liguleless1
AW433271|AW433271|sh54g07.y1 Gm-c1015 Glycine max
AW932595|AW932595|EST358438 tomato

15 AW096676|AW096676|EST289856 tomato
AJ011616|ZMA011616|Zea mays
AW036750|AW036750|EST252139 tomato
BF626329|BF626329|HVSMEA0018F24f Hordeum vulgare
AJ011614|ZMA011614|Zea mays

20 AJ011642|ATH011642|Arabidopsis thaliana
BE022435|BE022435|sm85h04.y1 Gm-c1015 Glycine max
X92369|AMSPB1|A. majus
AC015450|AC015450|Arabidopsis thaliana
AC079692|AC079692|Arabidopsis thaliana

25 AJ011632|ATH011632|Arabidopsis thaliana
AJ011631|ATH011631|Arabidopsis thaliana
BE455349|BE455349|HVSMEh0097E20f Hordeum vulgare
AJ242960|ATH242960|Arabidopsis thaliana
AJ011610|ATH011610|Arabidopsis thaliana

30 AJ132097|ATH132097|Arabidopsis thaliana
AL138658|ATT209|Arabidopsis thaliana
AJ011615|ZMA011615|Zea mays
BE499739|BE499739|WHE0975_ Wheat
AW398794|AW398794|EST309294 L. pennellii

35 AJ011618|ZMA011618|Zea mays
AW747167|AW747167|WS1_66_F11.bl_
AJ011577|ATH011577|Arabidopsis thaliana
AI992727|AI992727|701493410 A. thaliana
BE060783|BE060783|HVSMEg0013F15f Hordeum vulgare

40 BE804992|BE804992|ss34h10.y1 Gm-c1061 Glycine max
BE325341|BE325341|NF120H09ST1F1009

AC007369|AC007369|Arabidopsis thaliana
AJ011619|ZMA011619|Zea mays
BI099345|BI099345|IP1_37_H10.b1_A002
BI071295|BI071295|C054P79U Populus
5 AZ920400|AZ920400|1006019G01.y2 1006 -
AZ919034|AZ919034|1006013G02.x3 1006 -
BE805023|BE805023|ss35d09.y1 Gm-cl061 Glycine max
BG582086|BG582086|EST483824 GVN Medicago truncata
AJ011609|ATH011609|Arabidopsis thaliana
10 BE023083|BE023083|sm90e08.y1 Gm-cl015 Glycine max

Furthermore, the invention relates to modifying NDR-NHL-genes or gene products. All proteins belonging to this family contain one (and sometimes even more than one) transmembrane domain. *Arabidopsis* contains a large number of NDR-NHL genes, such as:

aad21459, aaf18257, aac36175, k10d20 (position 40852-41619),
aad21460, cab78082, aad21461, aad42003, aaf02134, aaf187656,
aad02133, cab43430, cab88990, cab80950, aad25632, aaf23842, a1163812,
20 f20d21-35, t13m11-12, f1e22-7, t23g18, f5d14-4266, t32f12-16, f11f19-
11, f11f19-12, f11f19-13, t20p8-13, f12k2, f23h14, k10d20-44043,
k10d20-12, t19f11-6, t19f11-5, t10d17-10, f22o6-150, f3d13-5, m3e9-
80, t25p22-30, mhf15-4, mhf15-5, mrn17-4, mlf18-9, mgn6-11994, mjj3-
9667, f14f18-60, At1g17620 F11A6, At5g11890 , At2g27080 , At5g36970 ,
25 mlf18 , At1g65690 F1E22 , At4g01110 F2N1 , At2g35980 f11f19 ,
At4g01410 F3D13 , At1g54540 F20D21 , At2g46300 t3f17 , At5g21130 ,
At3g11650 T19F11 , At5g06320 MHF15 , At5g06330 MHF15 , At2g01080
f15b18 , At2g35460 t32f12 , At2g27260 f12k2 , At2g35970 f11f19 ,
At5g53730 MGN6 , At5g22870 MRN17 , At4g09590 , At3g54200 , At1g08160
30 T6D22 , At5g22200 , At3g52470 , At2g35960 f11f19 , At3g52460 ,
At5g56050 MDA7, At3g20590 K10D20 , At1g61760 T13M11 , At3g20600
K10D20 , At1g13050 F3F19 , At3g11660 T19F11 , At3g44220 , At1g64450
F1N19 , At3g26350 F20C19 C , At4g05220 , At5g45320 K9E15 ,
At4g23930 , At4g13270 , At4g39740 , At1g45688 F2G19 W , At5g42860
35 MBD2 , At1g32270 F27G20 , At4g30660 , At2g45430 f4123 , At4g30650 ,
At1g69500 F10D13

and

40 ndr1, At2g27080; T20P8.13, At5g21130, At1g65690, At5g36970,

At1g54540, At5g06320, At5g11890, At1g17620, At3g11650, At2g22180,
At5g22870, At2g35980, At2g46300, At4g05220, At2g35460, At2g27260,
At4g01410, At5g22200, At1g61760, At3g52470, At5g53730, At4g01110,
At2g35960, At3g52460, At4g09590, At2g35970, At3g26350, At3g11660,
5 At3g44220, At1g08160, At2g01080, At5g06330, At5g56050, At3g20600,
NDR1, At3g54200, At3g20590, At4g39740, At1g32270 syntaxin, putative,
At1g13050, At5g45320, At3g20610, At4g26490, At5g42860, At1g45688,
At4g26820

10 NDR-NHL genes belong to a large family of which one of the
first identified is the defence-associated gene HIN1 (Harpin-
induced gene). HIN1 is transcriptionally induced by harpins
and bacteria, that elicit hypersensitive responses in tobacco.
It is thus believed that the genes of the invention also play
15 a role in the hypersensitive reaction. Especially (see also
chapter 8) since the genes of the invention bear relation to
brassinoid-like responses and since brassinoid pathway
compounds have been found to interact in this same defence
system in plants. Other plant species also contain members of
20 this large gene family, such as:

Plant homologs of the *Arabidopsis* NDR/NHL genes:

25 BG582276|BG582276|EST484016 GVN *Medicago truncata*
AV553539|AV553539|Arabidopsis thaliana
AC069325|AC069325|Arabidopsis thaliana
AV526693|AV526693|Arabidopsis thaliana
BG583456|BG583456|EST485208 GVN *Medicago truncata*
30 AW267833|AW267833|EST305961 DSIR *Medicago truncata*
BE997791|BE997791|EST429514 GVSN *Medicago truncata*
BG580928|BG580928|EST482657 GVN *Medicago truncata*
BF520916|BF520916|EST458389 DSIL *Medicago truncata*
AV544651|AV544651|Arabidopsis thaliana
35 AV543762|AV543762|Arabidopsis thaliana
AW559665|AW559665|EST314777 DSIR *Medicago truncata*
BG581012|BG581012|EST482741 GVN *Medicago truncata*
AV552164|AV552164|Arabidopsis thaliana
40 BE999881|BE999881|EST431604 GVSN *Medicago truncata*
AW031098|AW031098|EST274405 tomato

- AI998763|AI998763|701546833 *A. thaliana*
AW219286|AW219286|EST301768 tomato
BE124562|BE124562|EST393597 GVN *Medicago truncata*
AV540371|AV540371|*Arabidopsis thaliana*
- 5 AV539549|AV539549|*Arabidopsis thaliana*
BG647432|BG647432|EST509051 HOGA *Medicago truncata*
BE434210|BE434210|EST405288 tomato
BG725849|BG725849|sae42g02.y1 Gm-cl051 *Glycine max*
AP003247|AP003247|*Oryza sativa*
- 10 BE348073|BE348073|sp11a11.y1 Gm-cl042 *Glycine max*
AW508383|AW508383|si40c06.y1 Gm-r1030 *Glycine max*
AI856504|AI856504|sb40b07.y1 Gm-cl014 *Glycine max*
BE556317|BE556317|sq01b07.y1 Gm-cl045 *Glycine max*
AA713120|AA713120|32681 *Arabidopsis*
- 15 AV541531|AV541531|*Arabidopsis thaliana*
AI894456|AI894456|EST263911 tomato
AW704493|AW704493|sk53g11.y1 Gm-cl019 *Glycine max*
AW219298|AW219298|EST301780 tomato
BF425685|BF425685|ss03c11.y1 Gm-cl047 *Glycine max*
- 20 AV422557|AV422557|*Lotus japonicus*
BE190816|BE190816|sn79a08.y1 Gm-cl038 *Glycine max*
BG580331|BG580331|EST482056 GVN *Medicago truncata*
AV423251|AV423251|*Lotus japonicus*
AI896088|AI896088|EST265531 tomato
- 25 AV413427|AV413427|*Lotus japonicus*
AV426656|AV426656|*Lotus japonicus*
AV416256|AV416256|*Lotus japonicus*
AL385732|CNS0690I|*Medicago truncatula*
AB016877|AB016877|*Arabidopsis thaliana*
- 30 AV419449|AV419449|*Lotus japonicus*
AI486269|AI486269|EST244590 tomato
AV411690|AV411690|*Lotus japonicus*
AV419925|AV419925|*Lotus japonicus*
AV418222|AV418222|*Lotus japonicus*
- 35 AV409427|AV409427|*Lotus japonicus*
AC005287|AC005287|*Arabidopsis thaliana*
AV426716|AV426716|*Lotus japonicus*
AV411791|AV411791|*Lotus japonicus*
BG351730|BG351730|131E12 Mature tuber
- 40 BG046452|BG046452|saa54b12.y1 Gm-cl060 *Glycine max*
AI781777|AI781777|EST262656 tomato

BE451428|BE451428|EST402316 tomato
AI772944|AI772944|EST254044 tomato
AI895510|AI895510|EST264953 tomato
AW030762|AW030762|EST274017 tomato
5 AW218859|AW218859|EST301341 tomato
 BE203936|BE203936|EST396612 KV0 *Medicago truncata*
 AV410289|AV410289|Lotus japonicus
 AW032019|AW032019|EST275473 tomato
 AW030868|AW030868|EST274158 tomato
10 AV421824|AV421824|Lotus japonicus
 BG646408|BG646408|EST508027 HOGA *Medicago truncata*
 AF325013|AF325013|Arabidopsis thaliana
 AC007234|AC007234|Arabidopsis thaliana
 AW217237|AW217237|EST295951 tomato
15 AC034257|AC034257|Arabidopsis thaliana
 AW625608|AW625608|EST319515 tomato
 AW031064|AW031064|EST274371 tomato
 AF370332|AF370332|Arabidopsis thaliana
 AB006700|AB006700|Arabidopsis thaliana
20 AW035467|AW035467|EST281205 tomato
 AL163812|ATF14F18|Arabidopsis thaliana
 AI896652|AI896652|EST266095 tomato
 AI730803|AI730803|BNLGH17970 Cotton
 AW034775|AW034775|EST278811 tomato
25

The invention provides the insight that RKS proteins or functional equivalents thereof play part in a signaling complex (herein also called the RKS signaling complex) comprising molecules of RKS proteins, ELS (Extracellular Like SERK) proteins, NDR/NHL proteins and SBP/SPL (Squamosa Binding Protein) proteins, and the corresponding protein ligands (see for example table 3) whereby each of these proteins interplay or act in such a way that modifying genes, or modifying expression of genes, encoding ELS, RKS, NDR/NHL or SBP/SPL, proteins or said ligands may lead to functionally equivalent results (Figure 5. Two-hybrid interaction experiments have for example shown in vitro interaction between RKS 0 and NDR0/NHL28 and members of the SBP/SPL family. Here we show that in vivo the individual components of this signaling

complex are regulating identical processes, as based on functional genomics on transgenic plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex. ELS gene products 5 are derived from at least two different genes in the *Arabidopsis* genome. They show high homology on protein level with the corresponding transmembrane RKS gene products.

However, they lack a transmembrane domain while they do contain a signalling sequence at the N-terminal end. Therefore 10 these proteins are thought to be positioned within vesicles within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologues have been detected in other plant species (see list 15 on page 3). ELS proteins are involved in the heterodimerizing complex with the RKS transmembrane receptor at the outer membrane site. ELS molecules are either in competition or collaboration with RKS molecules involved in the high affinity binding of the ligand. The signal transmitted from the ligand onto the RKS proteins is then transported over the membrane 20 towards the N-terminal site of RKS protein, located on the other side of the membrane. The activation stage of the RKS molecule is changed, as a result of transphosphorylation by dimerizing receptor kinase dimerizing partners. Subsequently 25 the signal is transmitted to other proteins, one family of such proteins is defined as the SBP/SPL family of transcription factors, the other family of proteins is represented by the NDR/NHL members.

The different obvious phenotypes created by modifying the 30 RKS gene products could be effected by one process regulating all different effects in transgenic plants.

All the phenotypes observed can be effected by the process of brassinosteroid perception. In chapter 1, RKS genes 35 are clearly involved in plant size and organ size. Loss of RKS expression results in a dwarf phenotype, similar as observed with brassinosteroid synthesis mutants. It was already known in literature that the phenotypes observed from modifying the

RKS genes are also observed when modifying the brassinosteroid pathway genes and/or their regulation, thereby altering the amount and nature of the brassinosteroids in plants.

Literature which describes the phenotypic effects of modifying
5 teh brassionosteroid pathway can, amogst others, be found in:
Plant Journal 26: 573-582 2001; Plant Journal 1996 9(5) 701-
713, genetic evidence for an essential role of
brassinosteroids in plant development; J. Cell Biochem Suppl.
21a 479 (1995) ; Mandava 1988 Plant growth-promoting
10 brassinosteroids, Ann. Rev. Plant. Physiol. Plant Mol. Biol.
39 23-52; Plant Physiol 1994 104: 505-513; Cell 85 (1996) 171-
182; Clouse et al. 1993 J. Plant Growth Regul. 12 61-66;
Clouse and Sasse (1998) Annu. Rev. Plant Physiol. Plant Mol.
Biol 49 427-451; Sasse, Steroidal Plant Hormones. Springer-
15 Verlag Tokyo pp 137-161 (1999).

It is thus believed, without being bound to any theory,
that modification of the RKS genes will result in a
modification of the brassinosteroid pathway, thereby giving
the various phenotypes that are shown below.

20 "Functionally equivalent" as used herein is not only used
to identify the functional equivalence of otherwise not so
homologous genes encoding ELS, RKS, NDR/NHL or SBP/SPL
proteins, but also means an equivalent gene or gene product of
25 genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins in
Arabidopsis Thaliana, e.g. identifying a homologue found in
nature in other plants or a homologue comprising a deliberate
nucleic acid modification, such as a deletion, truncation,
insertion, or deliberate codon substitution which may be made on
30 the basis of similarity in polarity, charge, solubility,
hydrophobicity, and/or the amphipathic nature of the residues as
long as the biological activity of the polypeptide is retained.
Homology is generally over at least 50% of the full-length of
the relevant sequence shown herein. As is well-understood,
35 homology at the amino acid level is generally in terms of
amino acid similarity or identity. Similarity allows for
"conservative variation", i. e. substitution of one

hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Deliberate amino acid substitution may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. In a preferred embodiment, all percentage homologies referred to herein refer to percentage sequence identity, e.g. percent (%) amino acid sequence identity with respect to a particular reference sequence can be the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, without considering any conservative substitutions as part of the sequence identity. Amino acid similarity or identity can be determined by genetic programs known in the art.

'Plant cell', as used herein, amongst others comprises seeds, suspension cultures, embryos, meristematic regions, callous tissues, protoplasts, leaves, roots, shoots, bulbs, gametophytes, sporophytes, pollen and microspores. A target plant to be modified according to the invention may be selected from any monocotyledonous or dicotyledonous plant species, such as for example ornamental plants, vegetables, arable crops etc. 'Dicotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has two or more free or fused cotyledons. 'Monocotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has one cotyledon. 'Angiospermae' or flowering plants are seed plants characterized by flowers as specialized organs of plant reproduction and by carpels covering the ovaries. Also included are gymnospermae. Gymnospermae are seed plants characterized by strobili as specialized organs for plant reproduction and by naked sporophylls bearing the male or female reproductive organs, for example woody plants. 'Ornamental'

plants are plants that are primarily in cultivation for their habitus, special shape, (flower, foliage or otherwise) colour or other characteristics which contribute to human well being indoor as cut flowers or pot plants or outdoors in the man made landscape, for example bulbous plant species like *Tulipa*, *Freesia*, *Narcissus*, *Hyacinthus* etc. 'Vegetables' are plants that are purposely selected or bred for human consumption of foliage, tubers, stems, fruits, flowers or parts of them and that may need an intensive cultivation regime. 'Arable crops' are generally purposely bred or selected for human objectivity's (ranging from direct or indirect consumption, feed or industrial applications such as fibers) for example soybean, sunflower, corn, peanut, maize, wheat, cotton, safflower and rapeseed.

The invention provides a method for modulating a developmental pathway of a plant comprising modifying a gene encoding for a gene product or protein belonging to a developmental cascade or signaling complex comprising modifying at least one gene encoding a gene product belonging to the complex of RKS proteins, ELS proteins, NDR/NHL proteins, SBP/SPL proteins and ligand proteins. In one embodiment, the invention provides a method for modulating or modifying organ size. Plant or plant organ size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex with a method according to the invention is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating

cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth,

5 proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Use of a method according to invention for elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase for example the size of plant

10 organs, the growth rate, the yield of harvested crop, the yield of total plant material or the total plant size.

Decreasing the levels of endogenous RKS gene product is provided in order to decrease the size of plant organs, the growth rate, or the total plant size.

15 In another embodiment, the invention relates to cell division. The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery

20 are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides

25 herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and

30 RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent Herewith the invention provides a method for modulating the number of cells to be formed within an

35 eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes,

especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

5

In a further embodiment, the invention relates to the regeneration of apical meristem. Modification the levels of different RKS and ELS genes within plants allows the initiation and / or outgrowth of apical meristems, resulting 10 in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and IPT. Here we show that modulation of the endogenous levels of RKS genes results in 15 the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*.

Herewith the invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein 20 said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 25 gene or functional equivalent thereof. A direct application of such a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction. Regeneration can be induced after overexpression of for example RKS0 and ELS1; or 30 by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the corresponding expression cassettes in the plant genome. A further example of essentially identical 35 functions for for example ELS1 and RKS0 overexpressing plants is for example shown in the detailed description, example 3, where both transgenic constructs are able to induce the

regeneration capacity of in vitro cultured *Arabidopsis* callus. Another example comprises functional interaction between RKS and SBP proteins which was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter. At the tip of double overexpressing plants, embryostructures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signaling cascade, resulting in the reprogramming of developmental fate of a determined meristem. Furthermore, it is herein also shown that several RKS genes are able to regulate proper identity and development of meristems and primordia. The invention for example also relates to fasciation. Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific

promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type.

Identical phenotypes can be observed when transgenic plants are produced that contain the NHL10 cDNA under control of an enhanced 35S promoter. The resulting phenotype of the resulting flowers show that flower organ primordia are switched in identity, similar as observed for RKS10 and RKS13. These meristematic identity switches are normally never observed in *Arabidopsis* and the fact that two different classes of genes are able to display the same phenotypes in transgenic plants is a clear indication for a process in which both members of the RKS and the NDR/NHL families are involved. The invention also relates to root development. Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular

wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof.

Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of

5 for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for

10 example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between

15 plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant hormones, interaction with

20 the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between

25 plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or

30 the elongation of the root hairs, as mediated by ELS1 and RKS3.

In a further embodiment, the invention relates to apical meristem identity. All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue

and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating

5 plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell

10 comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene

15 comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases

20 in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

25 Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering.

Modulation of meristem identity in terminal primordia, like
30 for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows the formation of completely new types of flowers and fused fruitstructures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can
35 clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

In another embodiment, the invention relates to male sterility. Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more

introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

Furthermore, surprisingly we observe that NDR NHL gene products share homology with the family of syntaxins, involved in vesicle transport, positioning of cell wall formation and cytokinesis.

Table 1

Homology between members of the syntaxin family and the NDR NHL family

That syntaxins and NDR/HNL genes share large homology becomes even more clear when performing a database search using the following site:

http://mips.gsf.de/proj/thal/db/search/search_frame.html

5 searching for homologous sequences with the sequence At1g32270

gene code:

predicted function:

	At1g32270 syntaxin, putative	Syntaxin
10	At5g46860 syntaxin related protein AtVam3p (gb AAC49823.1)	Syntaxin
	At4g17730 syntaxin	Syntaxin
	At5g16830 syntaxin homologue	Syntaxin
	At3g11650 unknown protein	Putative syntaxin
15	At2g35460 similar to harpin-induced protein	Putative syntaxin
	At5g06320 harpin-induced protein-like	Putative syntaxin
	At2g35980 similar to harpin-induced protein	Putative syntaxin
	At1g65690 hypothetical protein	NDR HNL
	At4g05220 putative protein	Putative syntaxin
20	At3g05710 putative syntaxin protein AtSNAP33	Syntaxin
	At2g27080 unknown protein	NDR HNL
	At3g52470 putative protein	Putative syntaxin
	At1g61760 hypothetical protein	Putative syntaxin
25	At5g21130 putative protein	NDR HNL
	At3g52400 syntaxin-like protein synt4	Syntaxin
	At2g35960 putative harpin-induced protein	Putative syntaxin
	At5g06330 harpin-induced protein-like	Putative syntaxin
	At5g26980 tSNARE	Syntaxin
30	At5g36970 putative protein	Putative syntaxin
	At3g44220 putative protein	Putative syntaxin
	At3g03800 s-syntaxin-like protein	Syntaxin
	At2g35970 putative harpin-induced protein	Putative syntaxin
	At4g09590 putative protein	Putative syntaxin
35	At4g23930 putative protein	
	At1g61290 similar to syntaxin-related protein	Syntaxin
	At3g11660 unknown protein	Putative syntaxin
	At1g54540 hypothetical protein	Putative syntaxin
	At3g24350 syntaxin-like protein	Syntaxin
40	At5g22200 NDR1/HIN1-like	NDR HNL

	At1g11250 syntaxin-related protein At-SYR1	Syntaxin
	At5g53880	
	At3g11820 putative syntaxin	Syntaxin
	At3g54200	Putative syntaxin
5	At5g05760 t-SNARE SED5	Syntaxin
	At5g53730	Putative syntaxin
	At4g03330 SYR1-like syntaxin 1	Syntaxin
	At3g47910	
	At5g08080 syntaxin-like protein	Syntaxin
10	At5g11890	Putative syntaxin
	At1g17620	Putative syntaxin
	At2g22180	Putative syntaxin
	At5g22870	Putative syntaxin
	At2g46300	Putative syntaxin
15	At2g27260	Putative syntaxin
	At4g01410	Putative syntaxin
	At5g22200	Putative syntaxin
	At4g01110	Putative syntaxin
	At3g52460	Putative syntaxin
20	At3g26350	Putative syntaxin
	At1g08160	Putative syntaxin
	At2g01080	Putative syntaxin
	At5g56050	Putative syntaxin
	At3g20600	Putative syntaxin
25	At3g20590	Putative syntaxin
	At4g39740	Putative syntaxin
	At1g32270	Putative syntaxin
	At1g13050	Putative syntaxin
	At5g45320	Putative syntaxin
30	At3g20610	Putative syntaxin
	At4g26490	Putative syntaxin
	At5942860	Putative syntaxin
	At1g45688	Putative syntaxin
	At4g26820	Putative syntaxin

35

This observation provides the explanation for understanding
40 the mechanism by which the RKS / NDR-NHL complex functions.
Cell wall immobilized RKS gene products (containing the

extensin-like extracellular domain) respond to a local ligand signal, in combination with the heterodimerizing ELS protein(s) either as homodimers, as RKS heterodimers or in combination with the heterodimerizing ELS protein(s).

- 5 Predicted ligands for the RKS / ELS receptor binding consist of peptide ligands (based on the LRR ligand binding domain of this class of receptors). These ligands are normally produced as a pre pro protein. The N-terminal signal sequence is removed by the transport through the Golgi system and 10 allows modification of the ligand at this stage (e.g. glycosylation). The ligands can then be secreted after which further processing is possible (e.g. proteolytic cleavage, removal of sugar groups etc.) The resulting peptide, possibly as a monomer or a (hetero)dimerizing molecule binds the 15 transmembrane receptor complex with high affinity, resulting in transmission of the signal from the ligand through the transmembrane receptor component towards the other site of the membrane.
- One class of ligands interacting with the RKS and / or ELS 20 receptors consists of the family of pre(pro)proteins shown hereunder in table 3.

Table 3 Ligands within the RKS signaling complex (herein also called RKS/ELS ligand proteins)

For each ligand (A to N) the genomic structure before splicing and processing 5'- towards 3' is given. Exons are indicated in large letters; introns and surrounding sequences (including leader 5'-and trailer sequences 3') are indicated in small letters.
 Beneath each DNA sequence the amino acid sequence of the pre-pro-peptide is given. The first line represents the signal sequence
 10 The second (set of) lines represents the pro-peptide.
 The last line represents the conserved Cysteine motif.

A. Atlg22690

15 1 attaaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgctgcg tttcccttcatt
 61 ctatctctt cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac
 121 ataaactacc aaggatcaa gctaattgtaa aaattactct catttccacg taacaaattg
 181 agtagctta agatattgtt gaaacttaggt ttgaattttc ttcttcttct tccatgcac
 241 ctccggaaaaa agggaaccaa tcaaaactgt ttgcataatca aactccaaaca ctttacagca
 301 aatgcaatct ataactgtt attatccaa taaaaacctg tgatttatgt ttggctccag
 361 cgatgaaagt ctatgcattgt gatctctatc caacatgagt aattgttcag aaaataaaaa
 421 gtagctgaaa tggatctata taaagaatca tccacaagta ctatttcac acactacttc
 481 aaaaatacta ctcaagaaat ATGAAGAAGA TGAATGTGGT GGCTTTGTT ACGCTGATCA
 541 TCTCTTTCTC TCTGCTTTCTC CAGgtaaact gttaaaacca ttttcaagac taccttttct
 601 ctatccaga caaacccaaag taaaacaatg aaaaatctct ctggctttc atagGTACTT
 661 GCAGAGTTGT CATCATCCAG CAAACATGAA ACTTCCTCTG TTTCTCAGgt aagagtata
 721 caaaaacata ctaaacaacac ttcaagaga gtaataatata agggaaatgtt ggcttcttt
 781 ttttggtgt aatcagACGA ATGACGAGAA CCAAACATGG GCGTTTAAGA AACACATACCA
 841 CCATCGTCCA AGAACATCAGtt agtctactct ttcaacactc taattccctt gttctaagta
 901 ttttttttgc cccccacaaac cttttttta ttaaatgagc caattttat agATTGTGGG
 961 CATGCATGCG CAAGGAGATG CAGTAAGACA TCGAGGAAGA AAGTTTGTCAG CAGGCCTGT
 1021 GGAAGTTGTT GTGCCAAGTG TCAGTGTGTG CGGCCGGAA CCTCCGGCAA CACAGCATCA
 1081 TGTCCCTTGCT ACGCCAGTAT CGGTACACAT GGCAATAAAC TCAAATGTCC TTAAAagact
 1141 ttcatttttcaactatagt ctcatttttctt gattatgtt cttctttgt tatgttgcat
 1201 gtgtgatgtt tgagcttattt attatgttga ttgttgacat aattcaacta tataattttgt
 1261 atcgattccg aataataaga tgagtgtt tattggctat taagttttt ttttttttt
 1321 ttgggcacaa tggctattaa gttttaaaca ttcgttttta ttgttacaa aaaaacaacaa
 1381 agtttcatttttccatattaaac accaaaatctc catacatattt accaaaacccaa aaaaatacac
 1441 aaggggggaga gagaccaacg gtttttttgc cagatggc atcttttttgc agccgtcacc
 1501 gtttcttaga cttaaacagcc acaacacctt tataaaagctt cacgcgatcc ttcaacgcatt
 1561 ctgcggagg ccgagccacc ttattgttttgc gatcaaacaa caaaacttct tcaaaacgcatt
 1621 tcaatgcacaa aggc

 45 MKKMNVVAFVTLIISFLLLSQVIA

 ELSSSSNNETSSVSQTNDENQTAASFKRTYHHRPRIN

 CGHACARRCSKTSRKVKVCHRACGSCCAKQCQCVPPGTSGNTASCPYASIRTHGNKLKCP*

B. At1g74670

1 gaaaaaaaaaaga agaaaagata atggccgtta ttaatatagt tgaaaacttg aaactacttt
5 61 ttagtttgcata tataatatacg tagacttaggg atccagttga gtttcttct ttatttttag
121 ttgtgtttta tgtttgcattt tacgtttta tatgtaaata agatattttt cgaatttatgg
181 ttttattttgg gtagaaggtagt tagaatgtact taaacaatca agtggcagaa tgagatataat
241 aaagtaataat aataatgtat ccgttataaa cttattgtac atgtgaatga ggaagcttac
301 acacacacac cttctataaa tagtgcacaa aactgggtgt tacacacac acattcataa
361 atctctcaaa gtaagaacta agagctttac tacagtccctatctctcacatc atcttcctc
421 tctctcaaga gcttagtcATG GCCAAACTCA TAACTTCTTT TCTCTTACTC ACAATTTTAT
481 TCACTTTCGT TTGTCTCACT ATGTCAAAAG AAGCTGAGTA CCATCCAGAA AGTgttaagtt
541 ttatttttttt ggtaaaaatag aaagtgttaag ttttataattt cattcaatty ttttgcctt
601 tccctttctta ttattgtca taaatctaacc cccgcgtta aattttgttt tgaaattaaaa
661 cagTATGGAC CAGGAAGTCT GAAATCATAC Cgttaagtaaa aacttcttct tcttttatga
721 atcttggttc ttattatata tcaaataaaaa actcgattat catgattgca gAATGTGGAG
781 GACAATGCAC AAGGAGATGT AGCAACACAA AGTATCATAA GCCATGCATG TTCTCTGCC
841 AAAAGTGTG TGCTAAATGC CTTGTGTCC CTCCAGGCAC GTACGGCAC AAACAAGTGT
901 GTCCTTGTTA CAACACTGG AAGACTCAAC AAGGTGGACC AAAATGTCCTA TAAacaaaaaa
961 cattgagaga gaaaccccaa tctgtttctt attttatatta attatttcca gtatgtttt
1021 gttgtcgta tggttaaattt atagtgtttt tgcatggatcatttcatc gataaacaat
1081 atcatataaa atcttctatg ttctttcac gtttgcattt ttttgttgcgttcaatacac
1141 gaaatgtgtat tggacccctt aatttaggaat atataaaaattt ttatatttata attagataat
1201 ctttcgatata gttaaaattt caaggattac ttgttgcattt gttggacaa tctattttat
1261 attttacttt ctaaggttgt aataactatat cttaaaatgtt ttagacagag tcctaatgat
1321 tttagtataa ttgttactat ttagttacgc ttgcggaaattt tggactttt ccaaagtggatt
1381 ctatataat ttgattcaact aatctgcgtt tccttctatgt tttttacaat tatggagatt
1441 ttgcacat gat

30

MAKLITSFLLLTILFTFVCLTMS

35 KEEAEYHPESYGPGLKSYQ

CGGQCTRRCSNTKYHKPCMFFCQKCCAKCLCVPPGTYGNKQVCPCYNWNKTQQGGPKCP *

C. At1g75750

1 cacaactttt atacgcacca ccaaccgacc catttgaaa aagagaaaat aaaccacaaa
5 61 aacacacata aataatatgc tgataacaat gtcttaaaaa tctatttacc atttcttagta
121 atcaaatatctt attgcaaaaa atatttataa gaatacacaaat gaaaatatgat aaaatacaaa
181 tgatattctca attacctaaa aaatataaaa atgtcttact ttatttcag ccactgttgg
241 aaagtacttg caatcatc gtatTTGAA ttataaaaact cagaaacaat tattttccct
301 gaaaagttaa aacttttaat aagatattta taaaataaaa agaatagtct agaccggaaa
361 tggggtcggt tgtccatcca aaggagtgtc ataaatagaa ccctccaagt tctcattagg
421 acacaacaac taaaaccaca ttatcatta cagtctgatt tgagctaagt tctctcatca
481 taaaactctcc ttggaaatc ATGGCTATTT CAAAAGCTCT TATCGCTCT CTTCTCATAT
541 CTCTTCTTGT TCTCCAACTC GTCCAGGCTG ATGTCgtacg tcttttcat cacaactaa
601 ttataactcaa tataatattt atgtttcaaa acacatattt ctcacatgtt acaacaatata
661 tcttgcaggGA AAACTCACAG AAGAAAAAATG GTTACGCAA GAAGATCGgt aattataatga
721 tttttattaa acctaacgtt aaattttagag ttagatataat aatctgtgtt ttcttttctt
781 gtatataatag ATTGTGGGAG TGCCTGTGTA GCACGGTGCA GCCTTTCGAG GAGGCCGAGG
841 CTGTGTACA GAGCGTGCAG GACTTGCTGC TACAGGTGCA ACTGTGTGCC TCCGGGTACG
901 TACGGAAACT ACGACAAAGTG CCAGTGCTAC CCTAGCCTCA CCAACCCACGG TGGACGCCGC
961 AAGTCCCCAT AAgaagaac aaagctctta attgctgcgg ataatggac gatgtcggtt
1021 ttttagtatt tactttggcg tatataatgt gatcgaataa taaaacgagaa cgtagtgcgtt
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1321 tgataactac tagactagct gaggataaga atattgtatgt atatatttgc ggacaatttt
1381 gaatttataa taccatttt taatcacgac catataaaaa taattcttgc ttgcgttata
1441 atttgtgtta atacgataga gtagacaaat ga

30

MAISKALIASILLISLLVLQLVQA

35 DVENSOKKNGYAKKID
CGSACVARCRLSRRPRLCHRACGTCCYRCNCVPPGTGNYDKCQCYASLTTHGRRKCP*

D. At2g14900

1 ataaactaaca atgggtgagt ggagatgtgc ttttagtcaa gtggtaat atattgact
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 121 gttatggatt agaccgtatc gatctaaaga tgtcaaagaa aaaaaaatgt gtttgtttaa
 181 agtaaatatg tagatgtgg cggtttaatgt aaagttctta taatctatg ttactttttaa
 241 ttttcatgaa ttcttaatgt aaagttctta taatctatg ttactttttaa caaattgttaa
 301 ggattactt gaaatttggt atcgaattct aagacaataa caaaataaca atgactgaac
 10 361 aagtgtatcaa aacataatgg aagaataat actgcagttc tattaaataac taaaagaagg
 421 ggttagattgg cctataaaaag gagaataaag agaccacaag aaggcttattt attccgggac
 481 taaaagaaaacg caaaagaaaac ATGAAAATAA TAGTCTCCAT CTTAGTGTAA GCCTCTCTTC
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 661 gtcacaatttgc tttctttagt ctttcggttca cataagaaaa atttacaaa tattaactag
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 841 acatggctt agacgcaaaa tcttaaggg tatctacaca agtttggat gaataatttc
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 1081 ttcttagATGC TTTTGGTAGT GGCGCGGTAG CTCCGGCACC GCAGAGCAAA GATGGACCGG
 1141 CGTTAGAGAA ATGGTGTGGA CAGAAATGTG AAGGGAGATG CAAAGAACG GGGATGAAAG
 1201 ATCGGTGTT GAAGTATTGTG GGGATATGTG GCAAAGACTG TCAGTGTGTT CCTTCAGGCA
 25 1261 CTTATGGGAA TAAGCATGAA TGTGCTTGCT ATCGTGACAA GCTCAGTAGC AAAGGCACTC
 1321 CTAAATGTC TTGATcttat ttctttccaa ccaaaaattt aaataatgtg ataagagaga
 1381 tccagtaaac taatataaaa ctataatgg atcttttgtt tatgattttt ttttttcat
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 1501 ctaaaattat gtggaaatcg ataatgtttaa tgaatgatata aatataaag tcctcagttt
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 1681 tcattccaaat ttgttggtaa ccaatgttggatg agatggat gaggactaga agatagagag
 1741 gagaagaacg ttgttggtaa aataattatg atggatgtg gacaactttt aagagatttt
 1801 aaaaagactg actaacgtgt taggttccatc acgt

35

MKIIIVSILVILASLLISSLASATIS

40

DAFGSGAVAPAPQSKDGPALKEW

CGOKCEGRCKEAGMKDRCLKYCGICCKDCQCVPSTYGNKHECACYRDKLSSKGTPKCP*

E. At2g18420

35 MAVFRVLLASLLISLLVLDVFVA

DMVTSNDAPKID

CNSRCQERCSLSSRPNLCHRACGTCCARCNCVAPGTSGNYDKCPCYGSLLTHGGRRKCP*

F. At2g30810

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10	301 tattttaaaa taccttctat actatgc当地 ttttattttgt tataaataagg tttiacattg 361 atcctgaaat atatcataag aaaatcaaaaa gtgaaataag agatcaaAT GATGAAGCTC 421 ATAGTTGTC TTGTTATATC CAGTTTGTG TTTGCTACTC AATTTCCTAA Tgtaaaaatt 481 attattttttt tcttccat atgattttatg aatccagaga aataaaaggttt tttttttttt 541 gttgtatgt acagGGTGTGAT GAATTAGAGA GTCAAGCTCA AGCACCTGCA ATCCATAAAGG
15	601 tatattttaa ttataaaaaa tcaaaactgt aataaaaaat aataaaaaata ttacaacaag 661 aatatcaatg ttattttca aactacatcaa tttttaaaata ttatattgt aacacaatgt 721 tatatttata tcgtctccat tgatttgcatttcaaaatttg tttttgtat ccaaccaatt 781 tcagAATGGA GGAGAACGCT CACTTAAACC AGAAAGgtaaa ttgtttttaaa gatatttt 841 ttatatttat agtaaatgt tgatcaaaatc acaactttttttaattttat gttgatttt 901 atttttctga agAATGTCGA AAGGCATGTG AATATCGATG TTGCGGACCA TCTCACAGGA 961 ACCATGTTT GTTTTTTGC AACAAATGTT GAAACAAATG TTTGTTGTTG CCATCGGGAA
20	1021 CATATGGACA CAAAGAAGAA TGTCCTTGCT ACAATAATTG GACGACCAAA GAAGGTGGAC 1081 CAAAATGTCC ATGAAAacaa aaaaattgtaa aagcaaaataa aatcttcatcg ttgttattctc 1141 tcaataaaaaat ctatgtttt aatcccttgg tttcaataataa gaataataa tggatgtt 1201 ataattttctt ctatccaaa attaaatgtt aatgcacaaaat aatgttggaaat gacttggacc 1261 ttttcgtgtt agttttttctt tttcaatcagc aacaatttttag atttatattt tcacttctac 1321 aaacacaaaaa catggatgtctt cttaactctt catccaaaca aatgtcattt ctcttcttct 1381 ttttccaaac atttcacaaac aatattttccat atttatattctt aatgtatgtt ttttttttt 1441 tttttttttt ttagggccat tttttaaaatc ttgttgggtt agattggcccc atgaaatgtt 1501 gacatattttt aacatcttca aatattttttttttt aatgttgggtt aatgtatgtt ttttttttt 1561 tgctcttattttt aaaaatgttta aataaaaaataat aata
25	
30	

MMKLIIVVFVISSLLFATQFSNG

35 DELESQAQAPAIHKNGGEGLKPEE

CPKACEYRCSATSHRKPCLFCKNCNKCLCVPSGTYGHKEECPYCYNWTTKEGGPKCP*

G. At2g39540

1 taatgctata ctttaaatct ataatatata ttagatgtga cttaaggaat ttcaatagg
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5 121 tcatacggat ttcaaaaata tctcaaaatt gttgtaaagt catgttaattt gaaatgaatg
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241 ctttcaatac tagtattata ctacttactt agtcaaaaaa gtttatgaat atgggtttt
301 ctgtatgtta atatttttaa ctggaaaatag taccgacata acaagtaaag atatctttat
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421 agccacattt caccatcaact actttgtttt cgccatatactttaaattttgtt atacgttagca
481 aactctttcg agaaaacaag ATGAAGCTCG TGGTTGTACA ATTCTTCATA ATCTCTCTTC
541 TCCTCACATC TTCATTTCCT GTACTTCAA GTGCTGATTG GTgttaagtgt ttacttaatc
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661 attttacata tatatgtat aaatgaatta gcagCATGCG GTGGAAAGTG CAATGTGAGA
721 TGCTCAAAGG CAGGACACAA TGAAGAATGC CTCAAGTACT GCAATATATG TTGCCAGAAG
781 TGTAAATTGTG TTCCCTCGGG AACCTTTGGA CACAAAGATG AATGTCCCTG CTACCGTGAT
841 ATGAAAAAAACT CCAAAGGTGG ATCCAAGTGT CCTTGAacgt tctttgaaga tcctcatcac
901 atacatataa cttctacgtt ctatatgtgt ggaaatattttt atcacatctt atgtttggaa
961 tatataaaaat aaaatcaatg ccccaatgtt tggaaatattttaatgtata tcttaatata
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1141 ttgcggccgtt ttgttattttaat acaaagtaac atcggtctgttttgactttt tgaaaaccac
1201 agatccaaaaa actgtttact ttctcttaag agaaagcaaa gccgagttag tccaagcgag
1261 tttttagagaga ttctgttact cactaccggaa gaacgacgct atgtcagaga ccggcgtgtc
25 1321 aatcgatcttccac gaccgatcta agtcggagga agaagacgaa gaagagtatt ctccac

MKLVVVQFFIISLLLTSFSVLSSA

30 DSS

CGGKCNVRCSKAGQHEECLKYCNICCQKCNCVPSGTFGHKDECPCYRDMKN SKGGSKCP*

H. At3g02885 (GASA5)

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	61	cttaaactcg	cttattttcc	cctttctata	tacagatatt	atcatttagtg	acattttcat
	121	tttccaaaca	gagcgtttag	acactagtca	actacacaat	ataattttcc	aatttttctact
	181	gagagaaaat	tttttttttt	ttttttccaa	ggcaagagtt	tagtctttt	gttctctat
	241	cgtgggtaat	tagtggatt	taatttacac	tgttgagtt	tttgatcttg	ctaagagaca
10	301	aaaacgacaa	gtgtggtagc	taatttagaaa	ttaaaatgac	ctacttcccc	agaatcacgg
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	421	tttctctata	aatatcttta	atccgttta	ttgtttctta	agaatatttt	attggcaatc
	481	aagattttt	aaccaaaaaa	ATGGCGAATT	GTATCAGAAAG	AAATGCTCTT	TTCTTCCTGA
	541	CTCTTCCTT	TTTATTGTC	GTCTCCAACC	TCGTCAGgt	aaacactca	aaacagattc
15	601	agtttattaa	agtctgatgt	tgaaggttt	tatattatcag	gctgtcrtg	gaggttttttt
	661	tgaccaaaaagg	ctatacattc	cttaaaaattt	taatggctat	tagttttctg	atatttttttt
	721	tttatataata	tatgacagGC	TGCTCGTGGT	GGTGGCAAC	TCAAACCCCC	ACgtacggac
	781	tcaaaaactt	tgttgttca	tatgatcata	ttaattttatt	aatctactat	tattgtataat
	841	gttgataaaat	aaactttttaa	gttacacataa	tggtgtttat	tttggtaaat	gtcagtttttc
20	901	tagtataact	tatgtctgt	attataagca	tgaacataaa	gatctcaatg	atttttttttt
	961	tgtttgtttt	tgttgtatgt	ttttttgtat	ggaaacattca	attgttagAGT	GCAACTCAAA
	1021	GTGTAGCTTC	CGTTGTCAG	CAACATCACA	CAAGAACGCCA	TGCATGTTCT	TTTGCCCTCAA
	1081	GTGTTGCAAA	AAATGTCCTT	GTGTTCTCC	TGGCACTTTC	GGCAACAAAC	AAACTTGTCC
	1141	ATGTTACAC	AACTGGAAAGA	CTAAAGAAGG	CCGTCCCCAA	TGTCTTAA	actttttttt
25	1201	agatataattt	gataatattt	atctgtttt	ggattatcaa	acactacta	ctctgttttt
	1261	atctgtttt	acaaggttgc	gattttctc	tacatctttt	ttgtgtctt	tgctcttaac
	1321	tgttgtgttt	gttatactgt	taagcccgc	caatgtgtca	tggccgaact	tattatggtt
	1381	acatattttat	gaaatgggt	tcattatcaa	ttgatttgag	cctacaaaaaa	tgttagccata
	1441	aagccccattt	agttgttaatt	gttaatattt	cagtcataaa	tatgatttt	tatatctatg
30	1501	atttatctctt	agtggttgat	atgtttgtat	gttggaaagtca	tgttcttattt	gcttccacgg
	1561	ttttaaaaacc	atcaacttgtc	taaggctaaa	ttctaatattt	actgtgaaaa	acattatttta
	1621	cgtgcgtaat	tatataattt	tatgtatagg	ttttaattcc	attttttcc	aatagtgttt
	1681	tatgtcaaa					

35

MANCIRRNALFFLTLLFLLSVSNLVQAA

40 RGGGKLKPQQ

CNSKCSFRCSATSHKKPCMFFCLCCKKCLCVPPGTFGNKQTCPCYNNWKTKEGRPKCP*

45

I. At4g09600 (GASA3)

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5 61 aaaagaaaaac gcgtgaatcg aatgatgagt gttAACGTTc gatcgagatg ccaccaaattc
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181 gacatgtgga ctctactttg ggtggcatgt tcataatctt ccacatcacc atgtaaacgt
241 gaaaacaccc accacatca cttacatctc aaacacatgt cttcattatc gtacgtatc
301 caaaaaaaaaa aatgaaaaac taggtttatg gattcttattt cgcaatgtat aatatacacac
10 361 ttgtaaaaat aaaaatattt aataagcatt ataaataaaac ccaaagaggt gtttagattt
421 tatacttaat tgtagtact aataagagaa ttagagagaa tagtttata tcttcacgaa
481 aactgcattc tttttagac ATGGCAATCT TCCGAAGTAC ACTAGTTTA CTGCCTGATCC
541 TCTTCTGCCT CACCACTTT GAGGttcata acttttgcatt ttacttctcc atgaatcatt
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661 tcacGTTCAT GTTCATGCTG CTGAAGATTC ACAAGTCGGT GAAGGCGTAG TGAAAATTGg
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901 TTACCGCTGC AACTGTGTGC CACCAGGCAC CGCCGGGAAAC CACCACCTTT GTCCCTTGCTA
961 CGCCTCCATT ACCACTCGTG GTGGCCGTCT CAAGTGCCCT TAAacatata cacatacaga
1021 tgtgtgtata tgtctccgc gaccacacac gtacgtttat gttttaaagga caatagtatg
1081 tatgagcagc tataaacaat ccagaagttt atggttcatgt ttgaaactagt ataagttgt
1141 tgaactgtgc ttcttttgc caaccatctt tgctgtatgt tttagcaaccc tatttaataaa
1201 attagagatt acaaaaaaaaaa aatgaaaaaa tgttttaaaaaa acgtggattt tttttttttgg
1261 gattaaaaat taattttcat ttgggttgcatt ttgtcaataaa attagctaag ttttttataac
1321 taggccgtt aagatatgct gttttttttt tgataataga gttgccttag aagtttataaa
1381 ctgtaaatat ctaacttcac ttcaatctca caaacacacg aatcaacttc agcactaaga
1441 atcgaatttga ccagaactga aagaaagttt aagaaaagct gaatacagag aattttacgaa

30 MAIFRSTLVLLLILFCLTTF

ELHVHAAEDSQVGEVVKID

35 CGGRCKGRCSKSSRPNLCLRACNSCCYRCNCVPPGTAGNHHLCPYCAYASITTRGGRLKCP*

J. At4g09610 (GASA2)

5	1 ttaacagttt aaccataa tgtaaactc ggtagcat ttgggtgaa ttctacccct 61 ttaaccatac atactaaaga cgcagagaag ttcatatgg agttaatcg aaatagctaa 121 acttttaatt ggggttaaca tattttaa cacttaacat ttaatcttgg atctctcatt 181 ttttttttat taacaaaat aaattcatt tagaacccaa cgttcaaaa actcgtaatg 241 ttttcttatt aaatcttac tatagtcac acaaagaaaa actaggaca tgcgtaccc 301 caatttatata catggattat tatttttagt gtataatata gataaaaaat aaaaaacatt 361 tggtagccg ataggcgata gccactataa atataccaaa gaggtggat tatacatata 421 gccgtataac caaagaggt atcagataga aatgttcta atttttgtt caactcacg 481 aatttgcatg agttcgac ATGGCAGTCT TCCGAAGTAC ACTGGTTCTG TTACTATCA 541 TCGCTCTGTCT CACCACTTAT GAGgttata atatttttg tttttatag tcccccaaga 601 cacctgaa tatttacta aattcatgtt tattatgtaa tgactgtca ttctctttag 661 CTTCACGTCC ACGCTGCTGA TGGTGCAGAAG GTCGGTGAAG GCGTAGTGA AATCGgtatg 721 taaccctaac ttatataataa cacgttggta tataacttta tattttctgt gggtgcaact 781 ttttcccaac ttatataatac cttttgtat gagaatgtct caagcttttta atgagatgtt 841 atatctcgaa gaaggaaat atgaactaaa agtttggat ctcttgcata aaaaaataaa 901 cttttgatgg gttaaacgg attaaattag ttacatgtt ttgatgtatg tatgtatgt 961 ttagATTGT GGTGGGAGAT GCAAAGATAG ATGCAGCAAA TCTTCGAGAAA CGAACGCTATG 1021 CTTGAGAGCG TGCAACAGCT GTGTTCCCG CTGCAACTGT GTGCCACCTG GTACTTCTGG 1081 AAACACCCCAC CTTTGTCCTT GCTACGCCCT CATTAACCACT CACGGTGGCC GCCTCAAGTG 1141 CCCTTAAat tttttctgt tctgtttctg tttttacttc tattttcgat atatgtacat 1201 gtgtgtgtac gtgtgtatgt atacaatgt tcgtatgttt tgaggacaa aagtatgt 1261 atgagaagct ataaacttaa tagaagttga tggttatgcg tattatcaaa ccgtgtact 1321 tctgaacaac caatttcggg ttgttccaag tttggcaacc ctaaaataaaa aattcaaaaat 1381 gattggagac tactcgtaa tagacatttg aacagatgaa atctcggttac gttttatat 1441 tttttgaact gtaatattat tatgcagaaag cggttttgta atggccgac aaaaaaaaaaaag 1501 tgggttggta atggatgtatc ttccgtatcta ttctggaaat ggtctcaaaa agtagagtt 1561 agatctcaat acgaaaatgt acccttcgt ttgatttac aaagcctttt attttggaaa 1621 cgttaaatcc tcacttaggt ctctttt
---	--

35 MAVERSTLVLLIIVCLTY

ELHVHAADGAKVGEGVVKID

CGGRCKDRCSSRTKLCLRACNSCCSRCNCVPPGTSGNTHLCPCYASITTHGRLKCP**

K. At5g15230 (GASA4)

5	1 aaatattcac cctaaaatga atctaaaaat gtacaaaatc acaggaaaat aaaactaagc 61 agaaatgtcc taagaaaact aaagtttta aaaaataatc ttcaagaga tactccaact 121 ggtgttataa gcaaaaacttg atttatcaa aacaggttca tagtatttta tatttagtc 181 tataagctt ccttaaccac tggtggaaaac catctaccgc agtctatta ccaatagca 241 gtaataaaat gggactaaac ttggggcat acgtggata atataatgg aggataacag 301 tataatgtat atgtttgcc acagggataa attgatacg gcaaatgtgt gtatataatag 361 ctatattgc acatcattgg gtcctcaacc aaaaactcct ctctcagtag acttctttc 421 atacctaag agactaaaac tagtttgagg agatttagag gagttttgg ttctttggat 481 acaaatatcc caaatgtaaa ATGGCTAAGT CATATGGAGC TATTCCTCCT TTGACCCCTCA 541 TTGTCTCTTT CATGCTTCAA ACCATGGtta cactcttatt ttttttttct ttttcaatg 601 ttggaaaaata ttgaagata tatatttgat tttttccctt attgacgac gatatgagac 661 aaaaatgtgggt tctattttg tacttttagt tggaaatataat ttaattttagc ctttttaatg 721 aaattaattt tactgtttt tcctctctt tttttcggtt ttttagGTTA TGGCCTCAAG 781 TGGATCTAAT GTGAAGTGGA GCCAGGtca tttttttttt gaaatcgacta gtaatttact 841 tttaaactat attttatacc tatttttatac tggtaactta acggaaaatgtt atttaatgt 901 tacccctttt ggttaattttt cagAACGTT ATGGACCAGG AAGCCTGAAA CGTACCCGta 961 agtttttct tcacagctat tcttaacaa ttttttttta atctcataat cgacgaaaaaa 1021 taaaacaattc aagaaatctt ttatttggtt ataataaaaaaaa aaaataagca tttcagggtc 1081 agaaaaataag ttgaaagtga agtgttaagt ggactgtttg gtcagatccg tagactcaaa 1141 atatatttaga tattgacgaa attgccccctt aatatggtca tacagtcataa gcaaccacca 1201 atcttgagac ccacaaaaca gtaaaaaaaaaaa aagtcataatg atttccacta gattctgttg 1261 tttttttagt taataaaaaaaa ttttttaggtg ttaacattttt gatattgtttt gatattggaaa 1321 caaccagAAT GCCCATCGGA ATGTGATAGG AGGTGTAAAAA AGACACAGTA CCACAAGGCT 1381 TGCATTACGT TCTGCAACAA ATGCTGCAGG AAGTGTCTCT GTGTGCTCTC GGGTTACTAT 1441 GGGAAACAAAC AAGTTTGCTC CTGCTACAAAC AACTGGAAAAA CTCAAGAGGG TGGACCAAAA 1501 TGCCCTTGAA aaaaatcccc ttctgtccct ttttataataaaaatttca actataacta 1561 aatttcctt gatcaatgtt ttatctactt tattccataat gttgtatgt tatgtcactc 1621 cttttcgat tttgttctaa atcctaaaaaa aatagagagt ggcctatga atgatatttt 1681 tcatgaatac ttgttttctt aaagatattt tcccattcat ccaccaaaaaaa aaaagatatt 1741 ttccatttcg aaaaatgtaa tactataaag ggtaggca accaaataat acaattttaaa 1801 aaatttcctgc gaaagaagta tgcatatgtg gaaaagaggtg acattgggtc ttcggggca 1861 gtactaaaaaa gcccattttt gatttttcca agctttttac aaaaatcagt gttcttaacgc 1921 gattgtttgc tgccgcatac ttctttataa caagacttgg gctttgggca gttggaaata 1981 aataacgaca acgatatttt acaatcggt
10.	
15	
20	
25	
30	
35	

MAKSYGAIFLLTLIVLFMLQTMV

40 MASSGSNVKWSQKRYGPGSLKRTQ

CPSECDRRCKKTQYHKACITFCNKCCRKCLCVPPGYYGNKQVCSCYNNWKTQEGGPKCP**

45

L. At5g14920

MALSLLSVFIFHVFTNVVFAAS

45 NEESNALVSLPTPTLPSPSA
TKPPSPALKPPTPSYKPPTLP
TTPIKPPTTKPPVKPPTIPVT
PVKPPVSTTPPIKLPPVQPPTY
KPPTPTVKKPSVQPPTYKPPT
50 PTVKPPPTTSPVKPPTPPVQS
PPVQPPTYKPPTSPVKPPTTT
PPVKPPTTPEPVQPPTYNPPT
TPVKPPTAPPVKPPTPPPVRT
RID
55 CVPLCGTRCGQHSRKNCMRACVTCCYRCKCVPPGTYGNKEKGSCYANMKTRGGSKCP*

M. At5g59845

5 1 gacttgagta tgaatccaat aacccaaat ttatgcagat tttagaatac ttcttataaa
61 tcttaatga ataacacaaa actttaacat acttttaaca aatcttgatt gaataacaac
121 agattctaca tgacattna aatcaactaa accttttga aatcataaac caataacaac
181 cccttaggtt ttactatcc ctaatctt gaaacttgc gtaacttgc attagtgaa ttcttataaa
241 tgagaaaaca ttaattatcc ctaatctt gaaacttgc cccacaaaaa tcttataaaat
301 tgggacagat ggactagata acaagcgttt cacctactcc aaaatttccc tataagtaac
361 tcttttgc acctctttt ctcccaaaac catcaactctt tttgcattgt gtgaaaacctt
421 cgagtttctt cttcatcttc tcaaaggtaac aaactttctc caaacagatt attattaaaa
481 caatctcata aagaactacg ATGAAATTCC CGGCTGTAAA AGTTCTTATT ATCTCTTC
541 TCATCACATC TTCTTGTC ATACTCTCAA CCGCGGATTG GTgtaatat acacaatgc
601 ttttcttatt tttagatctt ttctcattag aaatttagct ttcttataaa aatttgtattg
661 tgatgatgaa ttaatttagCA CCATGCAGGAG GAAAATGCAA CGTGAGATGT TCAAAGGCAG
721 GAAGACAAAGA TAGGTGTCTC AAGTATTGTA ATATATGTTG CGAGAAGTGT AACTATTGTG
781 TTCCTTCAGG CACTTATGGA AACAAAGATG AATGCCCTTG TTACCGCGAT ATGAAGAACT
841 CCAAAGGCAC GTCCAAATGT CCTTGATcat gttcttaaga ttatccctt agacacaata
901 tcttgaatgt taaagattgt gcttgcattg taaaataatg agcttgcattt acttctatga
961 atgaatatgt gaaagattt gacaataaaa tgatttgatg tattaaaata ttcttgcattg
1021 agtttatatgt gtataatgtatgatgatgatgatgatgatgatgatgatgatgatgatgatgatg
1081 ataaatctac aacaatccaa tgatgaaaaa ttttactaag ttaactgatc agaaaacgtt
1141 attatgggtt agaatcttgc gtagatgatgatgatgatgatgatgatgatgatgatgatgatgatg
1201 tgtcaatgt gataaagtaa gaagccattt ctcaacacat gtagttgata gcaaaactaaa
1261 caaggctcaa gcattgaaat tggaaacgtct cgatagataa gattggctca agaaaagcaa
1321 gtgttttttg ttgtagaaaaa cagaaattgtt aattactgtc tacttt

30 MKFPAVKVLIISILLITSSLFILSTA

DSSP

CGGKCNVRCSKAGRQDRCLKYCNICCEKCNYCVPSGTYGNKDECPCYRDMKN SKTSKCP*

N. At3g10170

genomic structure before splicing and processing 5' - towards 3'
predicted orf sequences are underlined

5 CTGTTTCAGAAAATGGCAACAAACTTAGCATCATTGTTTCTCCATTG
TTGTGTTACATCTCTCTGTCTGCCATATGCATGTAAGTGTTCAACA
CTCTATTCCCTATGTCACATTATCAACTTATCTTATACTGTCCTG
10 ATAAAAACACAGCCTATATACTTGGAAATCTCTGCTCGACAAACCACAAACCA
CCACAGTCGCAACCACAACTGCCGATCACAAATAACTCTCAAGTGAGTTT
CTCGTTCATCACTACTCAAAGAGTTCATCGAATCTACAAAACCT
TTTTAACATCCTTGCATCTTGTGATTTGGCAGTACGGTACTACT
CAAGGCAGCTTCACCCCCAAGGTAAACCCACTGACTAGCCTAGTTTTA
15 ATTAATGTTGTGCTGAATGCGAAACTAAATCCGCTATTCCACCTTATT
AGAGTGCGGGCAAGGTGTGGAGATAGATGCTCGAATACACAATACAAGA
AGCCGTGTTGTTCTCTGC~~AA~~ATGTTGTAACAAGTGCTTG
CCCCCAGGTACTTATGCAATAAGCAAGTATGCTCTGCTATAACA
GAAGACCAAGAGCGGTGGACCAAAATGCCCTTAGTTCTCTTAATTA
20 CTTTAGCATAAAACTCCATGTAATTGTTAATCTACCTATCATAATTATA
TATGTATTGGACTCTCCATAATCACATCAGTTCTGTGATTATGACGT

Amino acid sequence of the predicted pre-pro-peptide
the first line represents the signal sequence
the second (set of) lines represents the the pro-peptide
the last line represents the conserved Cysteine motif.

MATKLSIIVFSIVVLHLLSAHMH

FLINVCAECETKSAIPPLLE

30 CGPRCGDRCSEN~~T~~QYKKPCLFFCNKCCNKCLCVPPGTYGNKQVCPCYNWKTSGGPKCP*

They consist of an N-terminal signal peptide, followed by a variable domain (involved in mobility or cell wall attachment) and a C-terminal domain with 12 conserved cystein residues.

5 The consensus of this last domain is:

C-C-RC-----C---C--CC- (R/K)C-CVP(P/S)GT-G(N/H)---C-CY-----G--KCP*

(-) = any amino acid;

(C) = conserved C-residue

10 (/) = either one or the other amino acid at this position;

* = stopcodon

Some members of this gene family have been described previously, and represent the GASA family in *Arabidopsis thaliana* (Plant Mol. Biol. 36 (1998)). Similar family members containing the same structural motifs are present in rice (like GASR1) and tomato (Plant Journal 2 (1992) 153-159; Mol. Gen. Genet. 243 (1994) Taylor and Scheuring). In *Arabidopsis*, the GASA gene family represents 14 different members, similar as the number for the RKS gene family. Our data on the similar phenotypes for RKS4 and GASA3 (figure 6) and the fact that there are similar numbers of ligands and receptors suggest that there is a single GASA ligand molecule interaction with a single RKS molecule. T-DNA knock out phenotypes observed with several of the other GASA peptide ligand genes also show modifications of organ and plant size like the appearance of extreme dwarf plants resembling brassinosteroid insensitive mutants. Co-localization of RKS genes and GASA ligands on the genome (see figure 4) could provide clues of molecular interactions between GASA molecules and RKS molecules (similar as for S locus proteins and S locus receptor kinases).

Furthermore, in the chapter discussing the effects of roots in RKS transgenic plants, it was shown that overexpression of RKS genes can result in the formation of lateral roots (figure 26). One of the GASA ligands is involved in the formation and/or outgrowth of lateral roots as discussed in Mol. Gen. Genet. 243, 1994, 148-157.

Intracellularly, this signal is transmitted onto membrane (but not necessarily plasma membrane) associated NDR-NHL proteins. At least some of the functions of the syntaxin-like NDR-NHL 5 proteins would thereby result in the regulation of vesicle transport and /or the positioning of new cell wall formation. Neighboring cells are known to influence and determine the developmental state and the differentiation of cells. In transgenic plants with RKS and / or NDR-NHL expression 10 cassettes the positioning of new cell walls is modified, resulting in abnormal neighboring cells, resulting in abnormal development of groups of cells like flower meristem primordia as observed and shown with RKS0, RKS13 and NHL10.

Table 2 overview of accessions numbers of RKS signal complex genes in *arabidopsis* and in rice:

	Gene code	contig	gene prediction in At database	<i>Oryza sativa</i> japonica contig	approximate position in bp around:
5	RKS0	At1g71830	f14o23	ok	OSJNBA0036B21
	RKS1	At1g60800	f8a5	ok	P0038C05
	RKS2	At5g65240	mgn23	ok	OJ1212_C08
	RKS3	At5g63710	mbk5	ok	see rks2
	RKS4	At2g23950	t29e15	wrong, exon missing	P0708B04
10	RKS5	At5g45780	mra19	wrong, exon missing	OJ1077_A12
	RKS6	At5g10290	wt e 23	ok	see rks2
	RKS7	At5g16000	ku e 24	ok	P0038C05
	RKS8	At1g34210	f23m19	ok	OJ1134_B10
15	different genes!				
	RKS10	At4g33430	en d 25	wrong, exon missing	see rks0
	RKS11	At4g30520	wu d 20	wrong, exon missing	see rks4
	RKS12	At2g13800	f13j11	wrong, exon missing	see rks10
	RKS13	At2g13790	f13j11	ok	P0633E08
	RKS14	At3g25560	mw12	wrong, exon missing	OSJNBB0015G09
20	ELS1	At5g21090	ch e 52	ok	36.000
	ELS2	possibly allelic variant of ELS1	no genomic sequence identified yet	see els1	36.000
	ELS3	At3g43740	by c 21	ok	P0003H10
					53.000
					see els1
					P0468B07
					52.000

Homology between aa sequences from *arabidopsis* proteins are compared with the rice databases using:
http://mips.gsf.de/proj/thal/db/search/search_frame.html
 protein sequences based on *Oryza sativa japonica* contig sequences.

Arabidopsis thaliana ELS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

ttactctcaaattcctttcgattccctctttaaacacctccgaaagctcac
ATGGCGTCTCGAAACTATCGGTGGAGCTTCGCAGCTCGTTAACCTAA
CCTTAGCTTGATTCACCTGGTGAAGCAAACCTCGAAGGAGATGCTCTA
15 CGCTCTCGCCGGAGTTGACAGATCCAGACCAGTCCTCCAGAGCTGGGAT
CCAACTCTTGTAACTCTGTACCTGGTCCATGTCACCTGTAACCAAGACA
ACCGCGTCACTCGTGTGGATTGGAAATTCAAACCTCTGGACATCTTGC
GCCTGAGCTTGGGAAGCTTGAACATTACAGTATCTAGAGCTCTACAAAAC
AACATCCAAGGAACTATACTTCCGAATTGGAAATCTGAAGAATCTCATCA
20 GCTTGGATCTGTACAACAACAACTTACAGGGATAGTTCCCACTTCTTGGG
AAAATTGAAGTCTCTGGCTTTTACGGCTTAATGACAACCGATTGACGGTC
CAATCCCTAGAGCACTCACGGCAATCCAAGCCTTAAAGTTGTGACGTCTC
AAGCAATGATTGTGTGGACAATCCCACAAACGGACCCTTGCTCACATTCC
25 TTTACAGAACTTGAGAACAACCCGAGATTGGAGGGACCGBAATTACTCGGT
CTTGCAAGCTACGACACTAACTGCACTGAacaactggcaaaacctgaaaat
gaagaattgggggtgacttgtaaagaacacttcaccacttatcaaatac
acatctactatgtataagtatatatgttagtccaaaaaaaaaaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS1

30 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich

repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

5

MASRNYRWELFAASL
TLTLALIHLVEANSEG

DALYALRRSLTDP

10 DHVLQSWDPTLVN

PCTWFHVTQNQDNRVTRV

DLGNSNLSGHLA

15 P ELGKLEHLQYLELYKNNIQGTI
PSELGNLKNLISLDLYNNNLTGIV
PTSLGKLKSLVFLRLNDNRLLTGPI
PRALTAIPSLKVVDVSSNDLCGTI
PTNGPFAHIPLQNFENNPRLEGPE

20

LLGLASYDTNCT

Arabidopsis thaliana ELS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 aaaattactcaaattcctattagattactcttcgacccgtatgcac
ATGGCGTCTCGAAACTATCGGTGGAGCTCTCGCAGCTCGTTAACCTCAA
CCTTAGCTTGATTACACCTGGTCGAAGCAAACTCCGAAGGAGATGCTCTTA
CGCTCTCGCCGGAGTTAACAGATCCGGACCATGTCCTCCAGAGCTGGGAT
CCAACCTCTGTTAACCTTGACCTGGTCCATGTCACCTGTAACCAAGACA
15 ACCGCGTCACTCGTGTGGATTGGGGATTCAAACCTCTGGACATCTGC
GCCTGAGCTTGGGAAGCTGAACATTACAGTATCTAGAGCTCTACAAAAAC
AACATCCAAGGAACTATACTCCGAACCTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAACAACAAATCTACAGGGATAGTTCCCACCTTTGGG
AAAATTGAAGTCTGGTCTTTACGGCTTAATGACAACCGATTGACGGGG
20 CAATCCCTAGAGCACTCACTGCCAATCCAAGCCTTAAAGTTGTGGATGTC
TAAGCAATGATTGTGTGGAAACAATCCAACAAACGGACCTTGCTCACAT
TCCTTACAGAACTTTGAGAACAAACCCGAGGTTGGAGGGACCGGAATTACTC
GGTCTTGCAAGCTACGACACTGACACTTGAagaaattggcaaaacctga
aaatgaagaattggggggacctttaatgacaacacttaccactttatcaaat
25 atcacatctactatgtataatgttatatatgttagtccaaaaaaaaatgaa
aatcgaaatgtatcatctggtctcaattgagaacttgaggctgtgt
atgaaaattaaagattgtactgtatgttcgggtgtggattctgagaagta
acatttgtattggatgtatcaagttgtctgcctgtctgcaaaaaaaaaa

30

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as 35 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain

contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be
5 involved in attachment to other proteins or structures within the cell wall.

MASRNYRWELFAASL

ILTLALIHLVEANSEG

10

DALYALRRSLTDP

DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

15

DLGNSNLSGHLA

P ELGKLEHLQYLQLYKNNIQGTI

PSELGNILKNLISLDLYNNNLTGIV

PTSLGKLKSLVFLRLNDNRLTGPI

20

PRALTAIPSLKVVDVSSNDLCGTI

PTNGPFAHIPLQNFENNPRLEGPE

LLGLASYDTNCT

25

Arabidopsis thaliana ELS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttctctccggc~~aaaacc~~**ATGGTGGCGAAAACAGTCGGCGGGAGCTTCTAGCAGCTT**
CCCTGATCCTAACCTTAGCTCTAATT~~CGT~~CTAACGGAA~~GCA~~ACTCCGAAGGGGACGCTC
TTCACGCGCTTCGCCGGAGCTTATCAGATCCAGACAATGTTGTCAGAGTTGGGATCAA
CTCTTGTTAACCTTGTACTGGTTCATGTCAC~~T~~GTAATCAACACC~~AT~~CAAGTCAC~~T~~C
GTCTGGATTGGGAATTCAA~~ACTT~~ATCTGGACATCTAGTAC~~CT~~GAA~~CT~~TGGGAAGCTTG
15 AACATTACAATATCTTGA~~ACT~~CTACAAA~~ACGAGATT~~CAAGGA~~ACT~~TAC~~CT~~TGAGC
TTGGAA~~AT~~CTGAAGAGTCTAATCAGTTGGATCTGTACAACA~~AA~~ATCTCACCGGGAAAA
TCCC~~AT~~CTTCTTGGAAAATTGAAGCGGCTTAACGAAA~~ACCGATT~~GACCGGT~~CT~~ATT~~C~~
CTAGAGAA~~CT~~CACAGTTATTCAAGCCTTAAAGTTGATGTCTCAGGGAA~~AT~~GATT~~T~~G
GTGGAA~~ACA~~ATTCCAGTAGAAGGACCTTTGAACACATT~~C~~TATGCAA~~AA~~ACTT~~G~~GAGAAC~~A~~
20 ACCTGAGATTGGAGGGACCAGAA~~ACT~~ACTAGGTCTT~~G~~CGAGCTATGACACCAATT~~G~~CACTT
Aaaaagaagttgaagaa

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS3 protein.

25 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a 30 leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be 35 involved in attachment to other proteins or structures within the cell wall.

MVAQNSRRELLAASL
ILTLALIRLTEANSEG

DALHALRRSLSDP
5 DNVVQSWDPTLVN

PCTWFHVTNCNQHHQVTRL

DLGNSNLSGHLV

10 P ELGKLEHLQYLELYKNEIQGTI
PSELGNLKSLISLDLYNNNLTGKI
P SSLGKLKRLNENRLTGPI
PRELTVISSLKVVDVSGNDLCGTI
PVEGPFEHIPMQNFENNLRLEGPE

15 LLGLASYDTNCT

Arabidopsis thaliana RKS0 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atttttatTTtatTTTactcttgttggTTaatgctaAtggTTaaaagggtt
atcgaaaaaaatgagtgagTTgtgtgaggTTgtctgtaaagtgttaatggTggTgat
ttcggaaagttagggTTtcggatctgaagagatcaaAtcaagattcgaaattacca
ttgttggTgaa**ATGGAGTCGAGTTATGTGGTGT**TTATCTTACTTCACTGATCTTACTT
CCGAATCATTCACTGTGGCTGCTTCTGCTAATTGGAAAGGTGATGCTTGATACTTTG
15 AGGGTTACTCTAGTTGATCCAAACAATGTCTGCAGAGCTGGGATCCTACGCTAGTGAAT
CCTTGCACATGGTCCATGTCACTTGCAACAACGAGAACAGTGTCAAAAGAGTTGATTG
GGGAATGCAGAGTTATCTGGCCATTTAGTTCCAGAGCTTGGTGTGCTCAAGAAATTGAG
TATTGGAGCTTACAGTAACAAACATAACTGGCCGATTCTAGTAATCTGGAAATCTG
ACAAACATTAGTGA GTTGGATCTTACTTAAACAGCTTCTCCGGTCCTATTCCGGAATCA
20 TTGGGAAAGCTTCAAAGCTGAGATTCTCCGGCTTAACAAACAACAGTCTCACTGGGTCA
ATTCCATGTCACTGACCAATATTACTACCCTCAAGTGTAGATCTATCAAATAACAGA
CTCTCTGGTTCAAGTTCCTGACAATGGCTCCTCTCACTCTCACACCCATCAGTTGCT
AATAACCTAGACCTATGTGGACCTGTTACAAGTCACCCATGTCCTGGATCTCCCCGTT
TCTCCTCCACCACCTTTATTCAACCTCCCCAGTTCCACCCCGAGTGGTATGGTATA
25 ACTGGAGCAATAGCTGGTGGAGTTGCTGCAGGTGCTGCTTGCCTTGCTGCTCCTGCA
ATAGCCTTGCTTGGTGGCGACGAAGAAGCCCACTAGATATTCTTCGATGTCCCTGCC
GAAGAAGATCCAGAAGTTCATCTGGACAGCTCAAGAGGTTTCTTGCAGGGAGCTACAA
GTGGCGAGTGA TGGTTAGTAACAAGAACATTGGCAGAGGTGGTTGGAAAGTC
TACAAGGGACGCTTGGCAGACGGAACCTTGTGCTGTCAAGAGACTGAAGGAAGAGCGA
30 ACTCCAGGTGGAGAGCTCCAGTTCAAACAGAAGTAGAGATGATAAGTATGGCAGTTCAT
CGAAACCTGTTGAGATTACGAGGTTCTGTATGACACCGACCGAGAGATTGCTTGTAT
CCTTACATGGCCAATGGAAGTGTGCTCGTCTCAGAGAGAGGCCACCGTCACAACCT
CCGCTTGA TGGCCAACGCGGAAGAGAAATCGCGTAGGCTCAGCTCGAGGTTGTCTAC
CTACATGATCACTGCGATCCGAAGATCATTACCGTGACGTAAAAGCAGCAAACATCCTC
35 TTAGACGAAGAATTGCAAGCGGTTGTTGGAGATTGCTGGAAAGCTTATGGACTAT
AAAGACACTCACGTGACAACAGCAGTCCGTGGCACCACCGTCACATCGCTCCAGAAATAT
CTCTCAACCGGAAATCTTCAGAGAAAACCGACGTTTCCGGATACGGAATCATGCTTCTA
GAAC TAATCACAGGACAAAGAGCTTCACTCGCTCGGCTAGCTAACGACGACGACGTC
ATGTTACTTGACTGGTGAAGGATTGTTGAAGGAGAAGAAGACTAGAGATGTTAGTGGAT
40 CCAGATCTCAAACAAACTACGAGGGAGAGAACTGGAACAAGTGAATACAAGTGGCGTTG

CTATGCACGCAAGGATCACCAATGGAAAGACCAAAGATGTCTGAAGTTGTAAGGATGCTG
GAAGGAGATGGGCTTGCGGAGAAATGGGACGAATGCCAAAAGTTGAGATTGAGGGAA
GAGATTGATTGAGTCCTAATCCTAACTCTGATTGGATTCTGATTCTACTTACAATTG
CACGCCGTTGAGTTATCTGGTCCAAGGTAaaaaaaaaaaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS0 protein.

Different domains are spaced and shown from the N-terminus

10 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MESSYVVFILLSLILLPNHSL
WLASANLEG

DALHTLRVTLVDP

35 NNVLQSWDPTLVN

PCTWFHVTCNNENSVIRV

DLGNAELSGHLV

40 P ELGVLKLNQYLELYSNNITGPI

PSNLGNLTNLVSLDLYLNNSFSGPI
PESLGKLSKLRFLRLNNNSLTGSI
PMSLTNITTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDICGPV

5

TSHPCPGSPPFSPPPP
FIQPPPVPSTPSGYGITG

AIAGGVAAGAAL

10 PFAAPAIAFAWW

RRRKPLDIFFDVPAEEDPE
VHLGQLKRFSLRELQVAS

15 DGFSNKNILGRGGFGKVYKGRLAD
GTLVAVKRLKEERTPGGELQFO
TEVEMISMAVRNLLRLRGFCM
TPTERLLVYPYMANGVASCLR
ERPPSQPPLDWPTRKRIALGSA

20 RGLSYLHDHCDPKIIHRDVKA
NILLDEEFEAVVGDFGLAKLMD
YKDTHVTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGINLLELI
TGQRAFDLARLANDDDVMLLDW

25 VKGLLKEKKLEMVDPDLQTN
EERELEQVIQVALLCTQGSPME
RPKMSEVVRMLE

GDGLAEKWDEWQKVEILREEIDLS

30 PNPNSDWILDSTYNLHAVELSGPR

Arabidopsis thaliana RKS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10	ccaaagtgttttaagaaggatATGGAAGGTGTGAGATTGTTGGTGTGGAGATT GGATTCTGGTTTGATGGTCTTGATATCTCTGCTACACTTCTCCTACTGGT GTAAACTATGAAGTGACAGCTTGGTGTGAAGAATGAATTGAATGATCCGTACAAA GTTCTGAGAATTGGGATGTGAATTCAAGTTGATCCTGTAGCTGGAGAATGGTTCTTGC ACTGATGGCTATGTCTCTCACTGGATCTCCTAGCCAAAGCTGTCTGGTACATTGTCT
15	CCTAGAACCGAACCTCACCTATTACAATCAGTGGTGTGAAAACAATGCAATCACT GGTCCAATTCCGAAACGATTGGGAGGTTGGAGAACGCTTCAGTCACCTGATCTTCGAAC AATTCAATTCCACCGGGGAGACCGGCCTCACTGGAGAACCTAAGAACTGAATTACTTG CGGTTAAACAATAACAGTCTTATAGGAACCTGCCCTGAGTCTATCCAAGATTGAGGGA CTCACTCTAGTCGACATTCTGATAACAATCTTAGTGGTTCGCTGCCAAAAGTTCTGCC
20	AGAACTTCAAGGTATTGTAATGCGTAATCTGTGGCCAAAAGCTGTTCAAAGTGT TCTGCTGTTCCGAGCCTCTCACGCTTCCACAAGATGGTCCAGATGAATCAGGAACCTCGT ACCAATGGCCATCACGTTGCTCTGCATTGCCGCAAGCTCAGTGCAGCATTGGTT TTCTTACAAGCGGAATGTTCTTGGTGGAGATATGCCGTAACAAGCAAATATTTTT GACGTTAATGAACAATATGATCCAGAAGTGAGTTAGGGCACTGAAGAGGTATACATTG
25	AAAGAGCTTAGATCTGCCACCAATCATTCAACTCGAAGAACATTCTCGGAAGAGGCCGA TACGGGATTGTGTACAAAGGACACTTAAACGATGGAACCTTGGTGGCTGCAACAGTCTC AAGGACTGTAACATTGCCGGTGGAGAACGACTTCAGACAGAACGAGACTATAAGT TTGGCTCTCATCGCAATCTCCTCCGGCTCCGGTTCTGTAGTAGCAACCAGGAGAGA ATTTTAGTCTACCCCTACATGCCAAATGGGAGTGTGCACTCACGCTAAAGATAATATC
30	CGTGGAGAGCCAGCATTAGACTGGTCGAGAAGGAAGAACGAGTAGCGGTTGGACAGCGAGA GGACTAGTTACCTACACGAGCAATGTGACCCGAAGATTATACACCGCGATGTGAAAGCA GCTAACATTCTGTTAGATGAGGACTTCGAAGCAGTTGTTGGTGAATTGGTTAGCTAAC CTTCTAGACCATAGAGACTCTCATGTCACAACCTGCACTCCGTGGAACTGTTGGCCACATT GCACCTGAGTACTTATCCACGGGTCACTCCTCAGAGAACGACTGATGTCTTGGCTTGGC
35	ATACTTCTCCTTGAGCTCATTACTGGTCAGAAAGCTTGTATTGGCAGATCCGCACAC CAGAAAGGTGAATGCTTGACTGGGTGAAGAACGCTGCACCAAGAACGGAAACTAAAGCAG TTAATAGACAAAGATCTAAATGACAAGTTCGATAGAGTAGAACCTGAAAGAACGTTCAA GTTGCGCTACTCTGCACTCAATTCAATCCATCTCATGACCGAAAATGTCAGAACGTTAG AAGATGCTTGAAGGTGACGGTTGGCTGAGAGATGGGAAGCGACGCAGAACGGTACTGGT
40	GAGCATCAGCCACCGCCATTGCCACCGGGATGGTAGTTCTCGCCGCGTGTGAGGTAT

TACTCGGATTATTCAGGAATCGTCTCTGTAGTAGAAGCCATTGAGCTCTGGGTCC
CGATGATTatgactcactgttttaaaaaa

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate

15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-

20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably

25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MEGVRFVVWRLGFL
VFVWFDFDISSATLSPTGVNYEV

TALVAVKNELNDP

35 YKVLENWDVNSVD

PCSWRMVSCTDGYVSSL

DLPQSLSGT

LSPRIGNLTYLQSVLQNNAITGPI

PETIGRLEKLQSLDLSNNNSFTGEI

PASLGELKNLYLRLNNNSLIGTC

5 PESLSKIEGLTLVDISYNNLSGSL

PKVSARTFK VIGNALICGPK

AVSNCSAVPEPLTL

PQDGPDSEGTRTNG

10

HHVALAFAASF

AAFFVFFTSGMFLWW

RYRRNKQIFFDVNEQYDPE

15 VSLGHLKRYTFKELRSAT

NHFNSKNILGRGGYGIVYKGHLND

GTLVAVKRLKDCNIAGGEVQFQ

TEVETISLALHRNLLRLRGFCS

20 SNQERILVVPYMPNGVASRLK

DNIRGEPALDWSSRRKKIAVGTA

RGLVYLHEQCDPKIIHRDVKA

NILLDEDFEAVVGDFGLAKLLD

HRDSHVTTAVRGTVGHIAPEYL

25 STGQSSEKTDVFGFGILLLELI

TGQKALDFGRSAHQKGVMLDW

VKKLHQEGKLKQLIDKDLNDKF

DRVELEEIVQVALLCTQFNPSH

RPKMSEVMKMLE

30

GDGLAERWEATQNGTGEHQPPPLPPGMVSSS

PRVRYYSDYIQESSLVVEAIELSGPR

35

Arabidopsis thaliana RKS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

Italics indicate the presence of an alternatively spliced gene product.

10

tcaattttggtagctttagaaaa**ATGGCTCTGCTTATTATCACTGCCTTAGTTAGT**
AGTTTATGGTCATCTGTGTCACCAGATGCTCAAGGGATGCATTATTGCGTTGAGGAGC
TCGTTACGTGCATCTCCTGAACAGCTTAGTGATTGGAACCAGAATCAAGTCATCCTGT
ACTTGGTCTCAAGTTATTGTGATGACAAGAAACATGTTACTCTGTAACCTGTCTTAC
15 ATGAACCTCTCCTCGGAACACTGTCTCAGGAATAGGAATCTTGACAACACTCTCAAGACT
CTTACATTGAAGGGAAATGGAATAATGGGTGGAATACCAGAACCCATTGAAATCTGTCT
AGCTTGACCAGCTTAGATTTGGAGGATAATCACTTAAC TGATCGCATTCCATCCACTCTC
GGTAATCTCAAGAACCTACAGTTCTCAGGACCTTGAGTAGGAATAACCTTAATGGTTCT
ATCCC GGATTCACTTACAGGTCTATCAAACACTGATAAAATTCTGCTCGACTCAAATAAT
20 CTCAGTGGTAGATTCTCAGAGTTTATTCAAAATCCAAAATACAATTTCACAGCAAAC
AACTTGAGCTGTGGTGGCACTTCCCGAACCTTGTGTAACCGAGTCAGTCCTCAGGT
GATTCAAGCAGTAGAAAAACTGGAATCATCGCTGGAGTTAGCGGAATAGCGGTTATT
CTACTAGGATTCTTCTTCTTCTGCAAGGATAAACATAAAGGATATAACGAGAC
GTATTTGTGGATGTTGCAAGGAACGAACTTAAAAAGGTTGATTCAGGTGAAGTGGAC
25 AGAAGGATTGCTTTGGACAGTTGAGAAGATTGCATGGAGAGAGCTCAGTTGGCTACA
GATGAGTTCACTGAAAAGAACATGTTCTCGGACAAGGAGGCTTGGAAAGTTACAAAGGA
TTGCTTCGGATGGCACCAAGTCGCTGTAAAAGATTGACTGATTTGAACGTCCAGGA
GGAGATGAAGCTTCCAGAGAGAACAGTTGAGATGATAAGTGTAGCTGTTCATAGGAATCTG
CTTCGCCTTATCGGCTTGTACAACACAAACTGAACGACTTTGGTGTATCCTTCATG
30 CAGAACATCTAAGTGTGCATATTGCTTAAGAGAGATTAAACCCGGGGATCCAGTTCTGGAT
TGGTTCAAGGAGGAAACAGATTGCGTTAGGTGCAGCACGAGGACTCGAACATCTCATGAA
CATTGCAACCGAACATCACACAGAGATGTGAAAGCTGAAATGTGTTACTAGATGAA
GACTTGAAGCAGTGGTGGTATTTGGTTAGCCAAGTGGTAGATGTTAGAAGGACT
AATGTAACCAACTCAGGTCCAGGAACAATGGTCATATTGCAACCAGAACATGTATATCCACA
35 GGGAAATCGTCAGAGAAAACCGATGTTTGGGTACGGAATTATGCTTCTGGAGCTTGTAA
ACTGGACAAAGAGCAATTGATTCTCGCGGTTAGAGGAAGAACATGATGTCTTATTGCTA
GACCATGTGAAGAAACTGGAAAGAGAGAACATAGTAGATAAGAACAGCTT
GATGAGGATTATAAAGGAAGAACATGAAATGATGATAACAGTAGCTGCTATGCACA
CAAGCAGCACCGGAAGAACGACCAGCGATGTCGGAAGTAGTAAGAACATGCTAGAAGGAGAA
40 GGGCTTGCAGAGAGATGGGAAGAGTGGCAGAACATTGAAAGTGACGAGACAAGAACAGTT

CAGAGGTTGCAGAGGAGATTGATTGGGTGAAGATTCCATTAATAATCAAGATGCTATT
GAATTATCTGGTGGAAGATAGaaacaaaaaa

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS2 protein.
Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
- 15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 3 complete and 2 incomplete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site
- 20 for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
- 25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions. Italics indicate an alternatively spliced gene
- 30 product.

MALLIITALVFSSL

WSSVSPDAQG

- 35 DALFALRSSLR
ASPEQLSDWNQNQVD

PCTWSQVICDDKKHVTsv

TLSYMFSS GTLSSGI
G ILTTLKTLTLKGNGIMGGI
PESIGNLSSLTSLDLEDNHLDRI
5 PSTLGNLKNLQFLTLSRNNLNGSI
PDSL TGGLSKLINILDSNNLSEI
PQSLFKIPKYN FTANNLSCGG

TFPQPCVTTESSPSGDSSSRKTG

10 IIAGVVSGIAVIL
LGFFFFFFC

KDKHKGYKRDVFVDVAGTNFKKGLISGE
15 VDRRIAFGQLRFAWRELQLAT

DEFSEKNVLGQGGFGKVYKGLLSD
GTKVAVKRLTDFERPGGDEAQFQ
REVEMISVAVRNLLRLIGFCT
20 TQTERILLVYPFMQNLSVAYCLR
EIKPGDPVLDWFRRKQIALGAA
RGLEYLHEHCNPKIIHRDVKA
NVLLDEDFEAVVGDFGLAKLVD
VRRTNVTTQVRGTMGHIAPECI
25 STGKSSEKTDVFGYGYGIMLLELV
TGQRAIDFSRLEEEEDDVLLDH
VKKLEREKLEDIVDKKLDEDY
IKEEVEMMIQVALLCTQAAPEE
RPAMSEVVRMLE

30 GEGLAERWEWQNLEVTRQEEFQ

RLQRRFDWGEDSINNQDAIELSGGR

Arabidopsis thaliana RKS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

aacggtaaaagtccatgatcctctcgaggattcattcaaagaaaattgc~~ttt~~tagatgg
10 aacaatcagaaaattgtatcttacaatgttc**ATGCC**TTAGCTTGTGGAAATCACTTCG
TCAACAACTCAACCAGATATCGAAGGAGGAGCTGTGCAGCTCAGAGATTGCTTAAT
GATTGAGCAATCGTCTAAAATGGACACCGCAGTTGTGAGCCCTGCTATAGTTGGTCT
TATGTTACCTGCAGAGGCCAGAGTGTGTGGCTCTAAATCTTGCCTCGAGTGGATTACA
GGAACACTCTCTCCAGCTATTACAAA**ACTGAA**GTTCTGGTTACCTTAGAGTTACAGAAC
15 AATAGTTATCTGGTGCCTTACCA**GATTC**TCTGGAAACATGGTTAATCTACAGACTTTA
AACCTATCAGTGAATAGTTCAGCGGATCGATA**CCAGCGAGCTGGAGTCAGCTCTG**AAT
CTAAAGCACTTGGATCTCATCCAATAATTAA**CAGGAAGC**ATCCAAACACAATTCTC
TCAATCCAAACATTG**ATTTTCAGGA**ACTCAGCTTATATGCGGTAAA**AGTTGA**TCAG
CCTTGTTCTTCAAGTTCTCGTCTCCAGTCACATCCTCCAAGAAAAAGCTGAGAGACATT
20 ACTTTGACTGCAAGTTGTGGCTTCTATAATCTATTCCCTGGAGCAATGGTTATGTAT
CATCACCATCGCGTCCGCAGAACCAAATACGACATCTTTTGATGTAGCTGGGGAAAGAT
GACAGGAAGATTCCCTTGACAACTAAA**CGATTCTCTTG**AGTCACTGAAATCCAGCTCGCA
ACAGATA**GGTTCAACGAGAGCA**ATTGATAGGACAAGGAGGATTGGTAAAGTATA**CAGA**
GGTTGCTTCCAGACAAA**ACAAAGTTG**CAGTGAACCGCTTGC**GGATTACTTCAGTC**CT
25 GGAGGAGAAGCTGTTCCAAAGAGAGATT**CAGCTCATAAGCGTTGC**GGTTCAAAAAAT
CTCTTACGCCTTATTGGCTTCTGCACAA**CTTC**CTCTGAGAGAA**ATCCTG**TTATCCATAC
ATGGAAA**ATCTTAGTGTG**CATATCGACTAAGAGATTGAAAGC**GGGAGAGGAAGGATTA**
GA**CTGGCCAACAGGAAGCGTGTAGCTT**GGTT**CAGCTCACG**TTAGAGTATCTACAC
GAACATTGTAACCCGAAGATCATAACCGCGATCTCAAGGCTGCAA**ACACATA**CTT**TAGAC**
30 AACAA**TTTGAGCCAGTTCTGGAGATT**CGTTAGCTAAGCTTGTGGACACATCT**CG**
ACTCATGTCACA**ACTCAAGTCCGAGGC**ACAATGGTCACATTGC**GCCAGAGTATCT**CTGC
ACAGGAAA**ATCATCTG**AAAAA**ACCGATGTTTGGT**TACGGTATAACGCTTCTGAGCTT
GTTACTGGTCAGCGCG**CAATCG**ATTTCACGCTTGGAAAGAAGAGGAAA**ATATTCT**CTTG
CTTGATCATATAAGAAG**TTGCTTAGAGAA**CAGAGACTTAGAGACATTGTTGATAGCAAT
35 TTGACTACATATGACTCCAAAGAAG**TTGAAACA**ATCGTTCAAGTGGCTTCT**CGCACA**
CAAGGCTCACCAGAAGATAGACCAGCG**ATGTCTGAA**AGTGG**TCAAAATGCT**CAAGGGACT
GGTGGTTGG**CTGAGAA**ATGG**ACTGA**ATGG**AAACA**CTTGAAGAAG**TTAGGAACAAAGAA**
GCATTGTTGCTTCCGACTTACCGG**CTACTTGGGATG**AAGAAGAAACCACCG**TGATCAA**
GAATCTATCCGATTATCGACAG**CAAGATGA**agaagaaacagagagagaaagatatctatg
40 aaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS3 protein.

5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a 10 leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 4 complete repeats of each 15 approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular 20 domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth 25 domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MALAFVGITSSSTQPDIEG

30

GALLQLRDSLNDSSNRL

KWTRDFVS

PCYSWSYVTCRGQSVVAL

35

NLASSGFTGTLS

P AITKLKFLVTLELQNNSLSGAL

PDSLGNMVNLQTLNLSVNSFSGSI

PASWSQLSNLKHLDSLSSNNLTGSI
PTQFFSIPTFEFSGTQLICGKS

5 LNQPCSSSRPLVTSSKKLRD

ITLTASCVASIIL
FLGAMVAMYHHH

10 RVRRRTKYDIFFDVAGEDDR
KISFGQLKRFSLREIQLAT

DSFNESNLIGQGGFGKVYRGLLPD
15 KTKAVAKRLADYFSPGGEAAFQ
REIQLISVAVHKNLLRLIGFCT
TSSEERILVYPYMEMNSVAYRLR
DLKAGEEGLDWPTRKRVAFGSA
HGLEYLHEHCNPKIIHRDLKAA
20 NILLDNNFEPVLGDFGLAKLVD
TSLTHVTTQVRGTMGHIAPEYL
CTGKSSEKTDVFGYGITLLELV
TGQRAIDFSRLEEEENILLLD
HIKKLLREQRLRDIVDSNLTTY
25 DSKEVETIVQVALLCTQGSPED
RPAMSEVVKMLQ

GTGGLAEKWTEWEQLEEVRNKEALLL

30 PTLPATWDEEETTVDQESIRLSTAR

Arabidopsis thaliana RKS4 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tcttccttccctctggtaatctaattctaaagtttc**A**TGGTGGTGATGAAGATATTCTCTGTTCTGTTACTACTATGTTCTCGTTACTTGTCTCTCTGAACCCAGAAAC
CCTGAAGTGGAGGC GTTGATAAACATAAAGAACGAGTTACATGATCCACATGGTGTTC
AAAAACTGGGATGAGTTCTGTTGATCCTGTAGCTGGACTATGATCTCTGTTCTCA
GACAACCTCGTAATTGGCTTAGGAGCTCCAAGTCAGTCTCTTCAGGAACCTTATCTGGG
15 TCTATTGGAAATCTCACTAACTTCGACAAGTGTCAATTACAGAACAAATAACATCTCCGGT
AAAATCCCACCGGAGATTGTTCTCTCCCAAATTACAGACTCTGGATTATCCAATAAC
CGGTTCTCCGGT GAAATCCCCGGTCTGTTAACCAGCTGAGTAATCTCAAATATCTGTTG
AACAAACAACTCATTATCTGGGCCCTTCCTGCTCTGTCTCAAATCCCTCACCTCTCT
TTCTTAGACTTGCTTATAACAATCTCAGAGGTCTGTTCTAAATTCTGCAAGGACA
20 TTCAATGTTGCTGGAACCCCTTGATTGTAAAAACAGCCTACCGGAGATTGTTAGGA
TCAATCAGTGCAAGCCCTTTCTGTCCTTACGTTCTCATCAGGACGTAGAACCAAC
ATATTAGCAGTTGCACTTGGTGTAGCCTGGCTTGCTGTTAGTGTAAATCCTCTCTC
GGGTTCAATTGGTATCGAAAGAAACAAAGACGGTTAACGATGCTCGCATTAACAAGCAA
GAGGAAGGGTTACTTGGGTTGGGAAATCTAAGAACGTTCACATTCAAGGAACTTCATGTA
25 GCTACGGATGGTTTAGTCCAAGAGTATTCTGGTGTGGTGGTTGGTAATGTCTAC
AGAGGAAAATTGGGGATGGACAGTGGTGCAGTGAAACGATTGAAAGATGTGAATGGA
ACCTCCGGGAACTCACAGTTCTGACTGAGCTGAGATGATCAGCTTAGCTGTTCATAGG
AATTTGCTTCGGTTAATCGTTATTGTGCGAGTTCTAGCGAAAGACTCTTGTTC
TACATGTCCAATGGCAGCGTCGCCTCTAGGCTCAAAGCTAACGCCAGCGTTGGACTGGAAC
30 ACAAGGAAGAACGATAGCGATTGGAGCTGCAAGAGGGTTGTTATCTACACGAGCAATGC
GATCCCAAGATTATTCAACCGAGATGTCAGGCAGCAAACATTCTCCTAGATGAGTATTT
GAAGCAGTTGGGGATTGGACTAGCAAAGCTACTCAACCACGAGGATTACATGTC
ACAACCGCGTTAGAGGAACGTTGGTCACATTGCACCTGAGTATCTCTCCACCGGTCA
TCATCTGAGAAAACCGATGTCTTGGGTCTAGCTAGAGCTCATCACAGGA
35 ATGAGAGCTCTCGAGTTGGCAAGTCTGTTAGCCAGAAAGGAGCTATGCTAGAAATGGGTG
AGGAAGCTACACAAGGAAATGAAAGTAGAGGAGCTAGTAGACCGAGAACTGGGACAACC
TACGATAGAATAGAAGTTGGAGAGATGCTACAAGTGGCACTGCTCTGCACACTAGTTCT
CCAGCTCACAGACCCAAATGTCTGAAGTAGTTGCTAGATGCTGAAGGAGATGGATTAGCT
GAGAGATGGGCTGCTTCACATGACCATTACATTTCTACCATGCCAACATGTCTTACAGG
40 ACTATTACCTCTACTGATGGCAACAAACCAACATCTGTTGGCTCCTCAGGATT

GAAGATGAAGATGATAATCAAGCGTTAGATTCAATGCCATGGAACTATCTGGTCCAAGG
TAGtaaatcttggacacagaaaagaaacagatataatccccatgacttcaattttgtt

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS4 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate

15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-

20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably

25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MVVMKLIKTMKIFSVLLLL
CFFVTCSLSSEPRNPEV

EALINIKNELHDP

35 HGVFKNWDEFSVD

PCSWTMISCSSDNLVIGL

GAPSQSLSGTLS

G SIGNLTNLRQVSLQNNNISGKI
PPEICSLPKLQTLDSLNNRFSGEI
PGSVNQLSNLQYLRLNNNSLSGPF
5 PASLSQIPHLSFLDLSYNNLRGPV
PKFPARTFNVAGNPLICKNS

LPEICSGSISASPL
SVSLRSSSSGRRTN

10 ILAVALGVSLGFAVSIL
SLGFIWY

RKKQRRLTMLRINKQEE
15 GLLGLGNLRSFTFRELHVAT

DGFSSKSILGAGGFGNVYRGKFGD
GTVVAVKRLKDVNNGTSGNSQFR
TELEMISLAVHRNLLRLIGYCA
20 SSERLLVYPYMSNGSVASRLK
AKPALDWNTTRKKIAIGAA
RGLFYLYEQQCDPKIIHRDVKA
NILLDEYFEAVVGDFGLAKLLN
HEDSHVTTAVRGTVGHIAPEYL
25 STGQSSEKTDVFGFGILLLELI
TGMRALEFGKSVSQKGAMLEW
VRKLHKEMKVEELVDRELGTTY
DRIEVGEMLQALLCTQFLPAH
RPKMSEVVQMEL

30 GDGLAERWAASHDHSHFYHANM
SYRTITSTDGNNQTKHLFG

SSGFEDEDDNQALDSFAMELSGPR

Arabidopsis thaliana RKS5 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctagagaattcttatacttttctacg**ATGGAGATTCTTGATGAAGTTCTGTTTA**
GGAATCTGGTTTATTATTACTCTGTTCTGACTCTGTTCTGCCATGGATAGTCTTTA
TCTCCCAAGGTGGCTGCCTTAATGTCAGTGAAGAACAAAGATGAAAGATGAGAAAGAGGTT
TTGTCTGGTTGGGATATTAACCTCTGTTGATCCTGTACTTGGAACATGGTTGGTTGTTCT
TCTGAAGGTTTGTGGTTCTCTAGAGATGGCTAGTAAAGGATTATCAGGGATACTATCT
15 ACTAGTATTGGGAATTAACTCATCTTCATACTTTGTTACTTCAGAATAATCAGTTAACT
GGTCCGATTCTCTGAGTTAGGCCAACTCTCTGAGCTTGAAACGCTTGATTATCGGGG
ATACGGTTAGTGGTCAAATCCCAGCTCTTTAGGGTCTTAACACTAAACTACTTG
CGGCTTAGCAGGAATCTTTATCTGGCAAGTCCCTCACCTCGTCGCTGGCCTCTCAGGT
CTTCTTCTGGATCTATCTTCAACAATCTAACGGACCAACTCCGAATATATCAGCA
20 AAAGATTACAGGAAATGCATTCTTGTTGGTCCAGCTTCCAAAGAGCTTGCTCAGATGC
TACACCTGTGAGAAATGCTGCAATCGATCTGCAGCGACGGGTTGTCGAAAAGGACAAT
AGCAAACATCACAGCTTAGTGTCTCTTGCAATTGGCATTGTTGTCCTTATCATC
TCCCTAATGTTCTCTCTGGTGCTTGGCATCGATCACGTCTCAAGATCACAC
GTGCAGCAAGACTACGAATTGAAATCGGCCATCTGAAAAGGTCAGTTTCGCGAAATA
25 CAAACCGCAACAAAGCAATTAGTCCAAGAACATTGGGACAAGGAGGGTTGGGATG
GTTTATAAAGGGTATCTCCAAATGGAACGTGGTGGCAGTTAAAGATTGAAAGATCCG
ATTATACAGGAGAAGTTCAGTTCAAACCGAAGTAGAGATGATTGGCTTAGCTGTCAC
CGTAACCTTACGCCCTTGGATTCTGTATGACCCCGGAAGAGAGAAATGCTTGTAT
CCGTACATGCCAAATGGAAGCGTAGCTGATCGTCTGAGAGATTGGAATCGGAGGATAAGC
30 ATTGCACTCGGCGCAGCTCAGGACTTGTAACTTGACCGAGCAATGCAATCCAAAGATT
ATTACAGAGACGTCAAAGCTGCAAATATTCTACTTGATGAGAGCTTGAAAGCAATAGTT
GGCGATTGGTCTAGCAAAGCTTGTAGACCAGAGAGATTCACATGTCACACTACCGCAGTC
CGAGGAACCATGGACACATCGCTCCGAGTACCTTCACTGGACAGTCCTCAGAGAAA
ACCGATGTTTCGGATTGGAGTACTAATCCTGAACTCATAACAGGTCTAAAGATGATT
35 GATCAAGGCAATGGTCAAGTTGAAAGGAATGATATTGAGCTGGTAAGGACATTGAAA
GCAGAGAAGAGATTGCAGAGATGGTGGACAGAGATTGAAGGGAGAGTTGATGATTG
GTGTTGGAGGAAGTAGTGGAAATTGGCTTGCTTGTACACAGCCACATCCGAATCTAAGA
CCGAGGATGTCTCAAGTGTGAAGGTACTAGAAGGTTAGTGGAACAGTGTGAAGGAGGG
TATGAAGCTAGAGCTCCAAGTGTCTAGGAACACTACAGTAATGGTCATGAAGAGCAGTCC
40 TTTATTATTGAAGCCATTGAGCTCTGGACCACGATGatagacttcatagtgtcttaac

tagtcttcttgatttgttcattgtcatggc

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS5 protein.

- 5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains no
10 leucine zipper motif, in contrast to the other RKS proteins. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues.
15 The fifth domain contains many serine residues, and is likely to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine /
20 threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein /
25 protein interactions.

MEISLMKFLFLGIWVYYYS

VLDHSVSAAMDSSLSPKV

30

AALMSVKNKMKDDE

KEVLSGWDINSVD

PCTWNMVGCSSEGFVVVS

35

LEMASKGLSGILS

T SIGELTHLHTLLLQNNQLTGPI

PSELGQLSELETLDLSGNRFSGEI

PASLGFLTHLNYLRLSRNLLSGQV

PHLVAGLSGLSFLDLSFNNLSGPT
PNISAK DYRKCISLWSSFPR

ALLRCYTCEKCCNR

5 SAATGLSEKDNSK

HHSLVLSFAFGIVV

AFIISLMFLFFWVLWH

10 RSRLSRSHVQQDYEF

EIGHLKRFSTFREIQTAT

SNFSPKNILGQGGFGMVKGYLPN

GTVVAVKRLKDPIYTGEVQFQ

15 TEVEMIGLAVHRNLLRLFGFCM

TPEERMLVYPYMPNGSVADRLR

DWNRRISIALGAA

RGLVYLHEQCNPKIIHRDVKAA

NILLDESFEAIVGDFGLAKLLD

20 QRDHSVTAVRGTIGHIAPEYL

STGQSSEKTDVFGFGVLILELI

TGHKMIDQGNGQVRKGMLSW

VRTLKAEKRFAEMVDRDLKGEF

DDLVLVEEVVELALLCTQPHPNL

25 RPRMSQVLKV

LEGLVEQCEGGYEARA

PASVSRNYSNGHEEQSFIIIEAIELSGPR

Arabidopsis thaliana RKS6 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

attgtttccttctttggatttctccttgatggaccagctcaattaatgagatgag
10 ATGAGAATGTTCAGCTTGAGAAGATGGCTATGGCTTACTCTCTTGCCTGT
TTATGCTCATTGTGTCAGATGCTCAAGGGGATGCACTGTTGCAGGATCTCC
TTACGTGCATTACCGAACATCAGCTAAGTGACTGGAATCAGAACCAAGTTAACCTTGCAC
TGGTCCCAGTTATTGTGATGACAAAAACTTGTCACTCTCTTACATTGTCAAGATATG
AACTTCTCGGGAACCTTGTCTCAAGAGTAGGAATCCTAGAAAATCTCAAGACTCTTACT
15 TTAAAGGGAAATGGAATTACGGGTGAAATACCAGAACAGACTTGGAAATCTGACTAGCTTG
ACTAGTTGGATTTGGAGGACAATCAGCTAACTGGCGTATACCATCCACTATCGGTAAAT
CTCAAGAAAATTCAGTTCTTGACCTTGAGTAGGAACAAACTTAATGGGACTATTCCGGAG
TCACTCACTGGTCTTCAAACCTGTTAACCTGCTGCTGATTCCAATAGTCTCAGTGGT
CAGATTCTCAAAGTCTGTTGAGATCCAAAATAATTTCACGTCAAACAACTTGAAT
20 TGTGGCGGTGTCACACTCACCCCTTGATCCGGTTGCCATTCAAGGTGATTCAAGC
AAGCCTAAAATGGCATTATTGCTGGAGTTGCTGGAGTTACAGTTGTTCTTTGGA
ATCTTGGTGTTCATGCAAGGATAGGCATAAAGGATATAGACGTGATGTGTTG
GATGTTGCAGGTGAAGTGGACAGGGAAATTGCATTGGACAGTTGAAAAGGTTGCATGG
AGAGAGCTCCAGTTAGCGACAGATAACTCAGCGAAAAGAATGTAATTGGTCAAGGAGGC
25 TTTGGGAAAGTTACAAAGGAGTCTCCGGATACACCCAAAGTTGCTGTGAAGAGATTG
ACGGATTCGAAAGTCCTGGTGGAGATGCTGCTTCAAAGGGAAAGTAGAGATGATAAGT
GTAGCTGTTCATAGGAATCTACTCCGTCTTATCGGGTTCTGCACCACACAAACAGAACGC
CTTTGGTTATCCCTCATGCAAGTCTAAGTCTGACATCGTCTGAGAGAGATCAA
GCAGGGCACCGGTTCTAGATTGGAGACGAGGAAACGGATTGCCTTAGGAGCAGCGCGT
30 GGTTTGAGTATCTTCAATGAAACATTGCAATCCGAAGATCATACATCGTATGTGAAAGCA
GCTAATGTGTTACTAGATGAAGATTGAAAGCAGTGGTTGGTATTTGGTTAGCCAAG
CTAGTAGATGTTAGAAGGACTATGTGACTACTCAAGTTGAGGAACAATGGGTACATT
GCACCAAGAATATTATCAACAGGGAAATCATCAGAGAGAACCGATGTTTGGGTATGGA
ATTATGCTTCTTGAGCTTGTACAGGACAACGCGCAATAGACTTTCACGTTGGAGGAA
35 GAAGATGATGTCTTGTACTTGACCACGTGAAGAAACTGGAAGAGAGAACGAGATTAGGA
CCAATCGTAGATAAGAATTGGATGGAGAGTATATAAAAGAAGAACGAGATGATGATA
CAAGTGGCTTGCTTGTACACAAGGTTACCCAGAACGACCGACAGTGTGATGTGAAGTT
GTGAGGAGTGTAGAAGGAGAACGGCTGCGGAGAGATGGGAAGAGTGGCAAAACGTGGAA
GTCACCGAGACGTATGAGTTGAACGGTTGCAGAGGAGATTGATTGGGTGAAGATTCT
40 ATGCATAACCAAGATGCCATTGAATTATCTGGTGAAGATGAccaaaaacatcaaacctt

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS6 protein.

Different domains are spaced and shown from the N-terminus
5 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each
10 separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain
15 contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown
20 function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single
25 leucine rich repeat, probably involved in protein / protein interactions.

MRMFSL

QKMAMAFATLLFFACLCSFVSPDAQG

30

DALFALARISLRALP

NQLSDWNQNQVN

PCTWSQVICDDKNFVTSL

35

TLSDMNFGSTLSSRV

GILENLKTLTLKGNGITGEI

PEDFGNLTSLSDLLEDNQLTGRI

PSTIGNLKKLQFLTLSRNKLNGTI
PESLTGLPNLLNLLDSNSLSGQI
PQSLFEIPKYNFTSNNLNCGG

5 RQPHPCVSABAHDSSPKTG

IIAGVVAGVTVVL
FGILLFLFC

10 KDRHKGYRRDVFDVAGE
VDRRIAFGQLKRFARRELQLAT

DNFSEKNVLGQGGFGKVYKGVLPD
TPKAVAKRLTDFESPAGDAAFQ

15 REVEMISVAVRNLLRLIGFCT
TQTERLLVYPFMQNLSLAHLR
EIKAGDPVLDWETRKRIALGAA
RGFEYLHEHCNPKIIHRDVKA
NVLLDEDFEAVVGDFGLAKLVD
20 VRRTNVTTQVRGTMGHIAPEYL
STGKSSERTDVFGYGIMLLELV
TGQRAIDFSRLEEDDVLLLH
VKKLEREKRLGAIVDKNLDGEY
IKEEVEMMIQVALLCTQGSPED
25 RPVMSEVVRMLE

GEGLAERWEEWQNVEVTRRHEFE

RLQRREFDWGEDSMHNQDAIELSGGR

Arabidopsis thaliana RKS7 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 acatcttgtttctgctcattcctctgttcaaca**ATGGAGAGTACTATTGTTATGATGA**
TGATGATAACAAGATCTTCCTTGGCTTCTGGGATTTATGCCTCTGCTCTCTG
TTCACGGATTGCTTCTCCTAAAGGTGTTAAC**TTGAAGTGC**AAGCTTGTGGACATAA
AAGCTTCATTACATGATCCTCATGGTGTCTGATAACTGGGATAGAGATGCTGTTGATC
CTTGTAGTTGGACAATGGTCACTTGTCTTCTGAAA**ACTTGTCA**TGGCTTAGGCACAC
15 CAAGTCAGAATTATCTGGTACACTATCTCCAAGCATTACCAACTTAACAAATCTCGGA
TTGTGCTGTTGCAGAACAAACATAAAAGGAAAATTCCCTGCTGAGATTGGTCGGCTTA
CGAGGCTTGAGACTCTGATCTTCTGATAATTCTTCCACGGTGAATTCCCTTTCA
TAGGCTATCTACAAAGCCTGCAATATCTGAGGCTTAACAACAATTCTCTCTGGAGTGT
TTCCTCTGTCACTATCTAATATGACTCAACTTGCCTTCTGATTATCATAACAACATC
20 TTAGTGGCCTGTTCCAAGATTGCTGCAAAGACGTTAGCATCGTGGAACCCGCTGA
TATGTCCAACGGGTACCGAACCAAGACTGCAATGGAACAACATTGATAACCTATGTCTATGA
ACTTGAATCAAACGGAGTTCTTATACGCCGGATCGAGGAATCACAAATGGCAA
TCGCTGTTGGATCCAGCGTGGACTGTATCTTATCGTGGTTGTTTC
TCTGGTGGAGACAAAGACATAACCAAAACACATTCTTGATGTTAAAGATGGGAATCATC
25 ATGAGGAAGTTCACTTGGAAACCTGAGGAGATTGGTTCAAGGGAGCTCAGATTGCGA
CCAATAACTTCAGCAGTAAGAACTTATTGGGAAAGGTGGCTATGAAATGTATACAAAG
GAATACTGGAGATAGTACAGTGGTTGCAGTGAAAGCTAAAGATGGAGGAGCATTGG
GAGGAGAGATTCAAGTTCAAGACAGAAGTTGAAATGATCAGTTAGCTGTTCATCGAAATC
TCTTAAGACTCTACGGTTCTGCATCACACAAACTGAGAAGCTCTAGTTATCCTTATA
30 TGTCTAATGGAAGCGTTGCATCTGAATGAAAGCAAAACCTGTTCTGACTGGAGCATAA
GGAAGAGGATAGCCATAGGAGCTGCAAGAGGGCTTGTATCTCCATGAGCAATGTGATC
CGAAGATTATCCACCGCGATGTCAAAGCAGCGAATATACTCTGATGACTACTGTGAAG
CTGTGGTTGGCGATTTGGTTAGCTAAACTCTGGATCATCAAGATTCTCATGTGACAA
CCCGGGTTAGAGGCACGGTGGTCACATTGCTCCAGAGTATCTCTCAACTGGTCAATCCT
35 CTGAGAAAACAGATTTGGCTTGGGATTCTCTTCTGAGCTTGTAAACCAGGACAAA
GAGCTTTGAGTTGGTAAAGCGGCTAACAGAAAGGTGTGATGCTTGTGATTGGTTAAAA
AGATTCAAGAGAAGAAACTTGAGCTACTTGTGGATAAAGAGTTGTGAAGAAGAAGA
GCTACGATGAGATTGAGTTAGACGAAATGGTAAGAGTAGCTTGTGACACACAGTACC
TGCCAGGGACATAGACCAAAATGTCTGAAGTTGTCGAATGCTGGAAGGGAGATGGACTTG
40 CAGAGAAATGGGAAGCTCTCAAAGATCAGACAGTGTTCAAAATGTAGCAACAGGATAA

ATGAATTGATGTCATCTCAGACAGATACTCTGATCTTACCGATGACTCTAGTTACTTG
TGCAAGCAATGGAGCTCTGGTCCTAGATGAAatctatacatgaatctgaagaagaaga
agaacatgcacatctgtttcttgaatcaagaggattttttttgtataatagagagg
ttttttggaggaaatgttgtctctgtactgtataggctgtgtgtaagaagtat
5 tactgcacttagggttaattcaaagttttcacataaaaaatgatttagttgcgttgaata
gagggaacacttggagatttcatgtatgaaatttggaaaaaaaaaaaaaaaaaaa

10 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS7 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

15 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

35

MESTIVMMMITRSFF
CFLGFLCLLCSSVHGLLSPKGVNFEV

QALMDIKASLHDP
HGVLDNWDRDAVD

PCSWTMVTCSSENFVG

5

LGTPSQNLSGTL
SPSITNLTNLRIVLLQNNNIKGKI
PAEIGRLTRLETLDLSDNFHGEI
PFSVGYLQLQYIQLNNNSLSGVF
10 PLSLSNMTQLAFLDLSYNNLSGPV
PRFAA KTFSIVGNPLICPT

GTEPDCNGTTLIPMSMNL
NQTGVPLYAGGSRNHKMA

15

IAVGSSVGTVSLIFIAVGLFLWW

RQRHNQNTFFDVKDGNHHE
EVSLGNLRRFGFRELQIAT

20

NNFSSKNLLGKGGYGNVYKGILGD
STVVAVKRLKDGGALGGEIQFO
TEVEMISLAVHRNLLRLYGFCI
TQTEKLLVYPYMSNGSVA
25 SRMKAKPVLDWSIRKRIAIGAA
RGLVYLHEQCDPKIIHRDVKA
NILLDDYCEAVVGDFGLAKLLD
HQDSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELV

30

TGQRAFEFGKAANQKGVMLDW
VKKIHQEKKLELLVDKELLKKSY
DEIELDEMVRVALLCTQYLPGH
RPKMSEVVRMLE

35

GDGLAEKWEASQRSDS
VSKCSNRINELMSSS

DRYSDLTDDSSLVQAMELSGPR

Arabidopsis thaliana RKS8 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 gtttttttttttaccctttggaggatctgggaggagaaatttgctttttggtaa
ATGGGGAGAAAAAGTTGAAGCTTGGTTGTCTGCTTAATCTCACTGCTTCTCTG
TTAATTCGTTATGGCTTGCCCTCTCTAACATGGAAGGTGATGCACAGCTTGAGA
GCTAACATCTAGTTGATCCAATAATGTCTTGCAAAGCTGGGATCCTACGCTTGTAAATCCG
TGTACTGGTTCACGTAACGTGTAACAACGAGAACAGTGTATAAGAGTCGATCTGGG
15 AATGCAGACTTGTCTGGTCAGTTGGTCCTCAGCTAGGTCAAGAACATTGCAGTAC
TTGGAGCTTATAGTAATAACATAACCGGGCCGGTCCAAGCGATCTGGGAATCTGACA
AACTTAGTGGAGCTGGATCTTACTTGAAACAGCTTCACTGGTCCAATTCCAGATTCTCTA
GGAAAGCTATTCAAGCTTCGCTTCTCGGCTAACAAATAACAGTCTCACCGGACCAATT
CCCATGTCATTGACTAATATCATGACCCCTCAAGTTGGATCTGTCGAACAAACCGATTA
20 TCCGGATCTGTTCTGATAATGGTCCTCTCGCTCTTCACTCCCACAGTTTGCTAAC
AACTTGGATCTATGCGGCCAGTTACTAGCCGTCCTGTCTGGATCTCCCCGTTTCT
CCTCCACCACCTTTATACCAACCTCCCATAGTTCTACACCAGGTGGGTATAGTGTACT
GGAGCCATTGCGGGAGGAGTTGCTGCTGGTGTCTTACTATTTGCTGCCCTGTTA
GCTTTGCTTGGTGGCGTAGAAGAAAACCTCAAGAATTCTCTTGATGTTCTGCCGAA
25 GAGGACCTGAGGTTCACTGGGGCAGCTTAAGCGTTCTCTACGGGAACCTCAAGTA
GCAACTGATAGCTTCAGCAACAAGAACATTGGGCCAGGTGGTGGGGTCTAC
AAAGGCCGTCTGCTGATGGAACACTTGTGTCAGTCAAACGGCTTAAAGAACAGCGAAC
CCAGGTGGCGAGCTCCAGTTCAAGACAGAAGTGGAGATGATAAGCATGGCGTTACAGA
AATCTCCTCAGGCTACGCGTTCTGTATGACCCCTACCGAGAGATTGCTTGTATCCT
30 TACATGGCTAATGGAAGTGTGCTTCTGTTGAGAGAACGTCCACCATCACAGTTGCCT
CTAGCCTGGTCAATAAGACAGCAAATCGCGTAGGATCAGCGAGGGGTTGTCTTATCTT
CATGATCATTGCGACCCAAAATTATTACCGTGATGTGAAAGCTGCTAATATTCTGTTG
GACGAGGAATTGAGGCGGTGGTAGGTGATTCGGGTTAGCTAGACTTATGGACTATAA
GATACTCATGTCACAACGGCTGTGCGTGGACTATTGGACACATTGCTCCTGAGTATCTC
35 TCAACTGGAAAATCTTCAGAGAAAATGATGTTTGGCTACGGGATCATGCTTTGGAA
CTGATTACAGGTAGAGAGAGCTTGATCTGCAAGACTGGCGAATGACGATGACGTTATG
CTCCTAGATTGGGTGAAAGGGTTTGAAGGAGAAGAAGCTGGAGATGCTTGTGGATCCT
GACCTGCAAAGCAATTACACAGAAGCAGAACAGCTCATAAGTGGCTTCTC
TGCACACAGAGCTCACCTATGGAACGACCTAACAGATGTCTGAGGTTGTCGAATGCTTGAA
40 GGTGACGGTTAGCGGAGAAATGGGACGAGTGGCAGAAAGTGGAGTTCTCAGGCAAGAA

G T G G A G C T C T C T T C A C C C C A C C T C T G A C T G G A T C C T T G A T T C G A C T G A T A A T C T T C A T
G C T A T G G A G T T G T C T G G T C C A A G A T A A a c g a c a t t g t a a t t g c c t a a c a g a a a a g a g a a
a g a a c a g a g a a a t t a a g a g a a t c a c t t c t g t a t t c t t

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS8 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30 MGRKKFEAFGFVCLISLLLLFNSL
WLASSNMEG

DALHSLRANLVDP
NNVLQSWDPTLVN

35 PCTWFHVTCNNENSVIRV

DLGNADLSGQLV
P QLGQLKNLQYLELYSNNITGPV
40 PSDLGNLTNLVSLDLYLNSFTGPI

PDSLGKLFKLRFLRLNNNSLTGPI
PMSLTNIMTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDLCGPV

5 TSRPCPGSPPFSPPPP
FIPPIIVPTPGGYSATG

AIAGGVAAGAAL
LFAAPALAFAWW

10 RRRKPOEFFFDVPAEEDPE
VHLGQLKRFSLRELQVAT

DSFSNKNILGRGGFGKVYKGRLAD
15 GTLAVKRLKEERTPGGELQFQ
TEVEMISMAVRNLLRLRGFCM
TPTERLLVYPYMANGVASCLR
ERPPSQLPLAWSIROQIALGSA
RGLSYLHDHCDPKIIHRDVCAA
20 NILLDEEFEAVVGDFGLARLMD
YKDTHVTTAVRGTIIGHIAPEYL
STGKSSEKTDVFGYGIMLLELI
TGQRAFDLARLANDDDVMLLDW
VKGLLKEKKLEMLVDPDLQSNY
25 TEAEVEQLIQVALLCTQSSPME
RPKMSEVVRMLE

GDGLAEKWDEWOKVEVLRQEVELS

30 SHPTSDWILDSTDNLHAMELSGPR

Arabidopsis thaliana rks10 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atcagggtttaacaatgatggatttctgtatgaggatagttctagggttttt
taatctcttgaggataaa**ATGGAACGAAGATTAATGATCCCTGCTTCTTGATT**
CTCGTTGGATTTGGTCTCAGAGTCGGCAACGCCAAGGTGATGCTAAAGTGCA
CTGAAAAACAGTTAGCCGACCCAATAAGGTGCTCAAAGTTGGATGCTACTCTGTT
ACTCCATGTACATGGTTCATGTTACTGCAATAGCGACAATAGTGTACACGTGTTGAC
15 CTTGGGAATGCAAATCTATCTGGACAGCTCGTAATGCAACTGGTCAGCTTCAAACATTG
CAGTACTTGGAGCTTATAGCAATAACATTACTGGGACAATCCCAGAACAGCTTGGAAAT
CTGACGAAATTGGTAGCTTGGATCTTACTTGAACAATTAAAGCGGGCTATTCCATCA
ACTCTCGGCCGACTTAAGAAACTCCGTTCTTGCCTTAATAACAATAGCTTATCTGGA
GAAATTCCAAGGTCTTGACTGCTGTCTGACGCTACAAGTTGGATCTCTCAAACAAT
20 CCTCTCACCGGAGATATTCTGTTAATGGTCTTTCACTTTCACTCCAATCAGTTT
GCCAACACCAAGTTGACTCCCTTCCATCTCCACCGCCTCTATCTCCTACACCG
CCATCACCTGCAGGGAGTAATAGAATTACTGGAGCGATTGCGGGAGGAGTTGCTGCAGGT
GCTGCACTCTATTGCTTCCGGCATTGCACTAGCTGGTGGCGAAGGAAAAGCCG
CAGGACCACCTTTGATGTACAGCTGAAGAGGACCCAGAAAGTTCAATTAGGACAATG
25 AAGAGGTTTCATTGCGTGAACCTACAAGTTGCTTCGGATAATTAGCAACAAGAACATA
TTGGGTAGAGGTGGTTGGTAAAGTTATAAAGGACGGTTAGCTGATGGTACTTTAGTG
GCCGTTAAAGGCTAAAGAGGAGCGCACCCAGGTGGCGAACTGCAGTTCCAGACAGAG
GTTGAGATGATTAGTATGGCGTTCACAGAAACTTGCTTCGGCTCGTGGATTGCGATG
ACTCCAACCGAAAGATTGCTTATCCCTACATGGCTAATGAAAGTGTGCCCTGT
30 TTAAGAGAACGTCCCGAGTCCCAGCCACCTTGATTGGCAAAGAGACAGCGTATTGCG
TTGGGATCTGCAAGAGGGCTTGCATTTACATGATCATTGCGACCCAAAGATTATTGAT
CGAGATGTGAAAGCTGCAAATATTGTTGGATGAAGAGTTGAAGCCGTGGTTGGGGAT
TTTGGACTTGCAAAACTCATGGACTACAAAGACACACATGTGACAACCGCAGTGCCTGG
ACAATTGGTCATATAGCCCCTGAGTACCTTCACTGGAAAATCATCAGAGAAAACCGAT
35 GTCTTGGGTATGGAGTCATGCTTCTGAGCTTACTGGACAAAGGGCTTTGATCTT
GCTCGCCTCGCGAATGATGATGATGTCATGTTACTAGACTGGGTGAAAGGGTTGTTAAA
GAGAAGAAATTGGAAGCACTAGTAGATGTTGATCTCAGGGTAATTACAAAGACGAAGAA
GTGGAGCAGCTAATCCAAGTGGCTTACTCTGCACTCAGAGTTACCAATGAAAGACCC
AAAATGTCTGAAGTTGTAAGAATGCTGAAGGAGATGGTTAGCTGAGAGATGGAAAGAG
40 TGGCAAAAGGAGGAAATGTTCAAGACAAGATTCAACTACCCAACCCACCATCCAGCGTG

TCTGGCTGGATCATTGGCGATTCCACTTCCCAGATCGAAAACGAATACCCCTCGGGTCCA
AGATAAgattcgaacacgaatgttttctgtat~~ttt~~gttttctctgtat~~ttt~~tatttag
ggtttttagcttc

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS10 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a
signal sequence. The second domain contains a leucine zipper motif,
containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues,
involved in disulphate bridge formation. The fourth domain contains a
leucine rich repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain contains many
serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain
contains a single transmembrane domain after which the predicted
intracellular domains are positioned. The seventh domain has an
unknown function. The eight domain represents a serine / threonine
protein kinase domain (Schmidt et al. 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth
domain has an unknown function. The last and tenth domain at the C-
terminal end represents part of a single leucine rich repeat,
probably involved in protein / protein interactions.

30 MERRLMIPCFFWLILVL
DLVLRVSGNAEG

DALSALKNSLADP
NKVLQSWDATLVT

35 PCTWFHVTCNSDNSVTRV

DLGNANLSGQLV
M QLGQLPNLQYLELYSNNITGTI
40 PEQLGNLTELVSLDLYLNNLSGPI

PSTLGRLKKLRFLRLNNNSLSGEI
PRSLTAVLTLQVLDSLNNPLTGDI
PVNGSFSLTPISFANTK LT PL

5 PASPPPPISPTPPSPAGSNRITG

AIAGGVAAAGAAL
LFAVPAIALAWW

10 RRKKPQDHFFDVPAEEDPE

VHLGQLKRFSLRELQVAS

DNFSNKNILGRGGFGKVYKGRLAD
GTLVAVKRLKEERTQGGELQFQ

15 TEVEMISMAVHRNLLRLRGFCM

TPTERLLVYPYMANGVASCLR

ERPESQQPLDWPKRQRIALGSA

RGLAYLHDHCDPKIIHRDVKAA

NILLDEEFEAVVGDFGLAKLMD

20 YKDTHVTTAVRGTIGHIAPEYL

STGKSSEKTDVFGYGVMLLELI

TGQRADFALARLANDDDVMLLDW

VKGLLKEKKLEALVDVDLQGNY

KDEEEVEOLIQVALLCTQSSPM

25 RPKMSEVVRMLE

GDGLAERWEWQKEEMFRQDFNYPTHH

PAVSGWIIGDSTSQIENEYPSGPR

Arabidopsis thaliana RKS 11 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttgttaacctctcgtaactaaaatcttcc**ATGGTAGTAGTAACAAAGAACCATGAAGA**
TTCAAATTCACTCCTTACTCGTCTTGTCCCTCTGTTCTACTCTCACTCTATCTT
CTGAGCCCAGAAACCCCTGAAGTTGAGGCCTGATAAGTATAAGGAACAATTGCATGATC
CTCATGGAGCTTGAACAATTGGGACGAGTTTCAGTTGATCCTGTAGCTGGCTATGA
TCACTTGCTCTCCGACAACCTCGTCACTGGACTAGGAGGCCAGCAGTCTCTCGG
15 GAGGTTATCTGAGTCTATCGAAATCTCACAAATCTCCGACAAGTGTCAATTGCAAATA
ACAACATCTCCGGCAAATTCCACCGAGCTCGGTTCTACCCAAATTACAAACCTTGG
ATCTTCCAACAACCAGATTCTCCGGTACATCCCTGTTCCATGACCAGCTAACAGGCC
TTCAATATCTGAGACTCAACAACAACTCTTGTCTGGCCCTCCCTGCTTCTTGTCCC
AAATTCCCTCACCTCTCCTTGTCTTACAACAATCTCAGTGGCCCTGTTCTA
20 AATTCCCAGCAAGGACTTTAACGTTGCTGGTAATCCTTGATTGTAGAACAGCAACCCAC
CTGAGATTTGTTCTGGATCAATCAATGCAAGTCCACTTCTGTTCTTGAGCTCTTCAT
CAGGACCGCAGGTCTAATAGATTGCAATAGCTCTAGTGTAAAGCCTGGCTCTGTTGTA
TACTAGTCCTTGCTCTGGCCTTTGTTGGTACCGAAAGAAACAAAGAAGGCTACTGA
TCCTTAACTTAAACGCAGATAAACAGAGGAAGGGCTCAAGGACTTGGGATCTAAGAA
25 GCTTCACATTCAAGAGAACTCCATGTTATACAGATGGTTCAAGTCCAAAGAACATTCTCG
GCGCTGGTGGATTGGTAATGTGTACAGAGGCAAGCTGGAGATGGGACAATGGTGGCAG
TGAAACGGTTGAAGGATATTAATGGAACCTCAGGGGATTACAGTTCTGTTGGCTAG
AGATGATTAGCTTAGCTGTTCATAGAAATCTGCTCGGTTAATTGGTTATTGCGCAACTT
CTGGTAAAGGCTTCTGTTACCCCTACATGCCATAATGGAAGCGTCGCCTCTAAGCTTA
30 AATCTAAACCGGATTGGACTGGAACATGAGGAAGAGGATAGCAATTGGTGCAGCGAGAG
GTTTGGTGTATCTACATGAGCAATGTGATCCAAAGATCATTGATAGAGATGAAAGGCAG
CTAATATTCTCTAGACGAGTGCTTGAAGCTGTTGGTACCTGGACTCGCAAAGC
TCCTTAACCAGCGGATTCTCATGTCACAAGCTGCGGTCGGTACGGTGGCCACATTG
CACCTGAATATCTCCACTGGTCAGTCTGAGAAAACCGATGTGTTGGGTTGGTA
35 TACTATTGCTCGAGCTCATAACCGGACTGAGAGCTCTGAGTTGGTAAACCGTTAGCC
AGAAAGGAGCTATGCTGAATGGGTGAGGAATTACATGAAGAGATGAAAGTAGAGGAAC
TATTGGATCGAGAACTCGGAACTAACATCGATAAGATTGAAGTGGAGAGATGTTGCAAG
TGGCTTGCTATGCACACAATCTGCCAGCTCATCGTCTAAATGTCTGAAGTTGTT
TGATGCTTGAAGGCATGGATTAGCCAGAGAGATGGCTGCTCGCATAACCATTCACT
40 TCTACCATGCCAATATCTCTTCAAGACAATCTCTGTCTACTACTTCTGTCTCAA

GGCTTGACGCACATTGCAATGATCCAACTTATCAAATGTTGGATCTCGGCTTCGATG
ATGACGATGATCATCAGCCTTAGATTCCCTTGCATGGA~~ACTATCCGGTCCAAGATAAc~~
acaatgaaagaaagatatcattttacgatggatcaaacaatccaatgaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS11 protein.

10 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).
At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a
15 leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each
20 approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular
25 domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
30 domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MVVVTKKTMKIQIHL~~LYS~~FLFL

35 CFSTLTL~~SSE~~PRNPEV

EALISIRNNNLHDP

HGALNNWDEF~~S~~V~~D~~

PCSWAMITCSPDNLVIGL

GAPSQSLSGGLS

5 ESIGNLTNLRQVSLQNNNISGKI
PPELGFLPKLQTLDLSNNRFSGDI
PVSIDQSSLQYLRRLNNNSLSGPF
PASLSQIPHLSFLDLSYNNLSGPV
PKFPARTFNVAGNPLICRSN

10 PPEICSGSINASPL
SVSLSSSSGRRSNR

LAIALSVSLGSVVIL
15 VLALGSFCWY

RKKQRRLLILNLNGADKQEE
GLQGLGNLRSFTFRELHVYT

20 DGFSSKNILGAGGFGNVYRGKLGD
GTMVAVKRLKDINGTSGDSQFR
MELEMISLAVHKNLLRLIGYCA
TSGERLLVYPYMPNGSVASKLK
SKPALDWNNMRKRIAIGAA

25 RGLLYLHEQCDPKIIHRDVKA
NILLDECFEAVVGDFGLAKLLN
HADSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELI
TGLRALEFGKTVSQKGAMLEW

30 VRKLHEEMKVEELLDRELGTNY
DKIEVGEMLQVALLCTQYLP
RPKMSEVVLMLE

35 GDGLAERWAASHNHSHFYHANI
SFKTISSLSTTSVSRDAHCNDPTYQMFG

SSAFDDDDHQPLDSFAMELSGPR

Arabidopsis thaliana RKS12 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tttaaaaacccgttagttctcaatttcatacgacttgc~~t~~tttagtcttagaagtggaaa
ATGGAACATGGATCATCCCGTGGTTATTGGCTGATTCTATTCTCGATTTGTTCC
AGAGTCACCGGAAAAACACAAGTTGATGCTCTCATTGCTCTAAGAACAGTTATCATCA
GGTGACCATAACAAATATACTCCAAAGCTGGAATGCCACTCACGTTACTCCATGTTCA
TGGTTTCATGTTACTTGCATAACTGAAAACAGTGTACTCGTCTTGACCTGGGAGTGCT
15 AATCTATCTGGAGAACTGGTGCCACAGCCTGCTCAGCTTCAAATTGCAAGTACTTGGAA
CTTTTAACAATAATATTACTGGGGAGATACTGAGGAGCTGGCAGTTGATGGAACTA
GTAAGCTTGGACCTTTGCAAACAAACATAAGCGGTCCCACCCCTCTCTGGCAAA
CTAGGAAAACCTCCGCTTCTTGCCTTTATAACAAACAGCTATCTGGAGAAATTCCAAGG
TCTTGACTGCTCTGCCGCTGGATGTTCTTGATATCTCAAACAAATCGGCTCAGTGGAGAT
20 ATTCCCTGTTAATGGTCCTTCGCAGTTCACTCTATGAGTTTGCCAATAATAATTAA
AGGCCGCGACCTGCATCTCCTTCACCATCACCTCAGGAACGCTGCAGCAATAGTAGTG
GGAGTTGCTGCAGGTCAGCACTCTATTGCGCTTGCTGGCTGAGAAGAAAAGT
CAGGGTCACTTTCTTGATGTACCTGCTGAAGAAAGACCCAGAGGTTATTAGGACAATT
AAAAGGTTCTCCTTGCCTGAAGGACTGCTAGTTGCTACAGAGAAATTAGCAAAAGAAATGTA
25 TTGGGCAAAGGACGTTTGGTATATTGTATAAAGGACGTTAGCTGATGACACTCTAGTG
GCTGTGAAACGGCTAAATGAAGAACGTACCAAGGGTGGGAACTGCAGTTCAAACCGAA
GTTGAGATGATCAGTATGGCGTTCATAGGAACCTGCTTCGGCTTCGTGGCTTTGCATG
ACTCCAACGTAAAGATTACTGTTATCCCTACATGGCTAATGGAAGTGTGCTTGT
TTAAGAGAGCGTCTGAAGGCAATCCAGCCCTGACTGCCAAAAGAAAGCATATTGCT
30 CTGGGATCAGCAAGGGGCTCGCATATTACACGATCATTGCGACCAAAAGATCATTCA
CTGGATGTGAAAGCTGCAAATATACTGTTAGATGAAGAGTTGAAGCTGTTGGAGAT
TTGGGCTAGAAAATTAAATGAATTATAACGACTCCATGTGACAACGTCTGTACGGG
ACGATTGCCATATAGGCCCGAGTACCTCTCGACAGGAAAATCTCTGAGAACACTGAT
GTTTTGGGTACGGGTATGCTCTCGAGCTCATCGACTGGACAAAAGGCTTCGATCTT
35 GCTCGGCTTGCAAATGATGATGATCATGTTACTCGACTGGGTGAAAGAGGTTTGAAA
GAGAAGAAGTTGGAAAGCCTTGTGGATGCAGAACACTCGAAGGAAAGTACGTGGAAACAGAA
GTGGAGCAGCTGATAAAATGGCTCTGCTCTGACTCAAAGTCTGCAATGGAACGTCCA
AAGATGTCAGAAGTAGTGAGAATGCTGGAAGGAGATGGTTAGCTGAGAGATGGAAGAA
TGGCAAAAGGAGGAGATGCCAATACATGATTTAACTATCAAGCCTATCCTCATGCTGGC
40 ACTGACTGGCTCATCCCCTATTCCAATTCCCTATCGAAAACGATTACCCCTCGGGGCCA

AGATAActttttagaaagggtcattcttgggttcaacaagtatata
gtgaagttgtaaaaccccacattcaccttgaatatcactactataa

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS12 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
leucine zipper motif, containing 2 leucine residues, each
15 separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
20 contains many serine and proline residues, and is likely to
contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
25 function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt et al. 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
30 leucine rich repeat, probably involved in protein / protein
interactions.

MEHGSSRGFI

WLILFLDFVSRVTGKTQV

35

DALIALRSSLSSGDHTNNILQ

SWNATHVT

PCSWFHVTCNTENSVTRL

DLGSANLSGELV

P QLAQLPNLQYLELFNNNITGEI

5 PEELGDLMELVSLDFANNISGPI

PSSLGKLGKLRFRLRFLYNNSLSGEI

PRSLTALP LDVLDISNNRLSGDI

PVNGSFSQFTSMRFA NNKLRPR

10 PASPSPSPSGGTS

AAIVVGVAAGAALLFALAWWL

RRKLQGHFLDVPAAEEDPE

15 VYLGQFKRFSLRELLVAT

EKFSKRNVLGKGRFGILYKGRLAD

DTLVAVKRLNEERTKGGELOFQ

TEVEMISMAVRNLLRLRGFCM

20 TPTERLLVYPYMANGSVASCLR

ERPEGNPALDWPKRKHIALGSA

RGLAYLHDHCDQKIIHLDVKAA

NILLDEEFEAVVGDFGLAKLMN

YNDSHVTTAVRGTIGHIAPEYL

25 STGKSSEKTDVFGYGVMLLELI

TGQKAFDLARLANDDDIMLLDW

VKEVLKEKKLESLVDAELEGKY

VETEVEQLIQMALLCTQSSAME

RPKMSEVVRMLE

30

GDGLAERWEWQKEEMPIHDFNYQAY

PHAGTDWLIPYSNSLIENDYPSGPR

35

Arabidopsis thaliana RKS13 cDNA

The start codons encoding predicted the methionine residue of the gene product has been indicated by bold capitals. The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

taataaacctctaataataatggcttgctttactctgatgacaaggtcaaaaATGGAA
10 CAAAGATCACTCCTTGCTCCTTATCTGCTCTACTATTCAATTCACTCTCAGAGTC
GCTGGAAACGCTGAAGGTGATGCTTGACTCAGCTGAAAAACAGTTGTCATCAGGTGAC
CCTGCAAACAATGTACTCCAAAGCTGGATGCTACTCTTGTACTCCATGTACTTGGTT
CATGTTACTTGCAATCCTGAGAATAAAGTTACTCGTGTGACCTTGGGAATGCAAAACTA
TCTGGAAAGTTGGTCCAGAACCTGGTCAGCTTTAAACTGCAGTACTGGAGCTTAT
15 AGCAATAACATTACAGGGGAGATACTGAGGAGCTGGCGACTTGGTGGAACTAGTAAGC
TTGGATCTTACGCAAACAGCATAAGCGTCCCATCCCTCGTCTTGGCAAACTAGGA
AAACTCCGGTCTTGCCTAAACAACATAGCTTACAGGGAAATTCCAATGACTTTG
ACTTCTGTGCAGCTGCAAGTTCTGGATATCTCAAACAATCGGCTCAGTGGAGATATTCT
GTAAATGGTTCTTTCGCTCTTCACTCCTATCAGTTTGCAGATAATAGCTAACGGAT
20 CTTCCCGAACCTCCGCCTACTTCTACCTCTCCTACGCCACCACCTCAGGGGGCAA
ATGACTGCAGCAATAGCAGGGGAGTTGCTGCAGGTGCAGCACCTTCTATTGCTGTTCCA
GCCATTGCGTTGCTTGGCTCAGAAGAAAACCACAGGACCACTTTTGATGTACCT
GCTGAAGAAGACCCAGAGGTCATTTAGGACAACCTAAAAGGTTACCTTGCCTGAACTG
TTAGTTGCTACTGATAACTTAGCAATAAAATGTATTGGTAGAGGTGGTTGGTAAA
25 GTGTATAAAGGACGTTAGCCGATGGCAATCTAGTGGCTGTCAAAGGCTAAAGAAAGAA
CGTACCAAGGGTGGGAACTGCAGTTCAAACCGAAGTTGAGATGATCAGTATGGCGTT
CATAGGAACCTGCTCGGCTTCGTGGCTTGCATGACTCCAACGTGAAAGATTACTGTT
TATCCCTACATGGCTAATGGAAGTGTGCTTCTGTTAAGAGAGCGCTGAAAGGCAAT
CCAGCACTTGCATTGGCCAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGCTTGC
30 TATTTACATGATCATTGCGACCAAAAATCATTACCGGGATGTTAAAGCTGCTAATATA
TTGTTAGATGAAGAGTTGAAGACTGTTGGAGATTTGGCTCGCAAATTAATGAAT
TATAATGACTCCCCTGACAACGTGACTGCTGACGGTACAATTGCCATAGGCCCGAG
TACCTCTCGACAGGAAAATCTCTGAGAAGACTGATGTTTGGTACGGGTCATGCTT
CTCGAGCTCATCACTGGACAAAAGGCTTCGATCTGCTCGGCTTGCACGAAATGATGATGAT
35 ATCATGTTACTCGACTGGGTGAAAGAGGTTTGAAGAGAAGAGAAGTGGAAAGCCTTGTG
GATGCAGAACTCGAAGGAAAGTACGTGGAAACAGAAGTGGAGCAGCTGATACAAATGGCT
CTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCAAAGATGTCAGAAGTAGTGAGAATG
CTGGAAGGAGATGGTTAGCTGAGAGATGGAAAGAATGGCAAAGGAGGAGATGCCAATA
CATGATTTAACTATCAAGCCTATCCTCATGCTGGCACTGACTGGCTCATCCCTATTCC
40 AATTCCCTTATCGAAAACGATTACCCCTGGGTCCAAGActtttagaaagggtctt

ttcttggtgggttcttcaacaagtatatacatatagattggtaagtttaagatgcaaaaaaa

aa

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS13 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as 10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains leucine zipper motifs, containing 2 times 2 leucine residues, each separated by seven other amino acids. The third domain 15 contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to 20 contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine 25 protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein 30 interactions.

MEQRSLLCFLYLL
LLFNFTLRVAGNAEG

35

DALTQLKNSLSSGDP
ANNVLQSWDATLVT

PCTWFHVTCNPENKVTRV

DLGNAKLSGKLV

P ELGQLLNQYLELYSNNITGEI

PEELGDLVELVSLDLYANSISGPI

5 PSSLGKLGKLRFRLNNNSLSGEI

PMTLTSVQLQV LDISNNRLSGDI

PVNNGSFSLFTPISFANNSLTDLPE

PPPTSTSPTPPPPSG

10

GQMTAAIAAGGVAAGAAL

LFAVPAIAFAWWL

RRKPQDHFFDVPGAEEDPE

15 VHLGQLKRFTLRELLVAT

DNFSNKNVLGRGGFGKVYKGRLAD

GNLVAVKRLKEERTKGGELOFQ

TEVEMISMASHRNLLRLRGFCM

20 TPTERLLVYPYMANGVASCLR

ERPEGNPALDWPKRKHIALGSA

RGLAYLHDHCDQKIIHRDVKA

NILLDEEFEAVVGDFGLAKLMN

YNDSHVTTAVRGTIGHIAPEYL

25 STGKSSEKTDVFGYGVMLLELI

TGQKAFDLARLANDDDIMLLDW

VKEVLKEKKLESIVDAELEGKY

VETEVEQLIQMALLCTQSSAME

RPKMSEVVRMLE

30

GDGLAERWEEWQKEEMPIHDFNYQA

YPHAGTDWLIPYSNSLIENDYPSGPR

35

Arabidopsis thaliana RKS14 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctgcaccc~~ttagagattaactctcaagaaaaacaagtttgattcggacaaag~~ATGTTG
CAAGGAAGAAGAGAAAGCAAAAAAGAGTTATGCTTGTCTCTCAACTTCTTCTTC
TTTATCTGTTTCTTCTTCTCTGCAGAAC~~T~~CACAGACAAAGTTGTTGCCCTAATA
GGAATCAAAGCTCACTGACTGATCCTCATGGAGTTCTAATGAATTGGGATGACACAGCA
GTTGATCCATGTAGCTGGAACATGATCACTTGTTCTGATGGTTTGT~~CATAAGGCTAGAA~~
15 GCTCCAAGCCAAA~~ACTTATCAGGA~~ACTCTTCATCAAGTATTGAAATTAA~~ACAA~~ATCTT
CAA~~ACTGT~~TATACAGGTTATTGCAGAAC~~A~~ATTACATAACAGGAAACATCCCTCATGAGATT
GGGAAATTGATGAA~~ACTCAA~~ACACTTGATCTCTACCAATAACTCACTGGTCAAATC
CCATTCACTTTCTTACTCCAAA~~ATCTT~~CACAGGAGGGTAATAATAACAGCCTGACA
GGAACAATT~~CCTAGCT~~CATTGGCAACATGACCCAACTCACTTTGGATT~~TGTGT~~TAT
20 AATAACTTGAGTGGACCAGTTCCAAGATCACTGCCAAACATTCAATGTTATGGCAAT
TCTCAGATT~~TGT~~CCAACAGGA~~ACTGAGAA~~AGACTGTAATGGACTCAGCCTAAGCCAATG
TCAATCAC~~CTT~~GAACAGTTCTCAAAGAA~~ACTAAA~~ACCGGAAATCGGGTAGTCTT~~CGGT~~
GTAAGCTTGACATGTGTTGCTTGT~~GATCATTGG~~CTTGGTTCTTCTTGGGAGA
AGAAGACATAACAA~~ACAAGT~~TATTATTCTTGACATTAATGAGCAAACAAAGGAAGAAATG
25 TGTCTAGGGAATCTAAGGAGGTTAATTCAAAGAAC~~TTCAATCCGCAACTAGT~~AACTTC
AGCAGCAAGAATCTGGTCGGAAAAGGAGGGTTGGAAATGTGTATAAAGGTTGTCTTCAT
GATGGAAAGTATCATCGCGGTGAAGAGATTAAAGGATATAACAA~~ATGGTGG~~GAGAGGTT
CAGTT~~CAGACAGAG~~CTTGAATGATAAGCCTGCCGTCCACCGGAATCTCCTCCGCTTA
TACGGTTCTGTACTACTTCC~~CTCGT~~GAACGGCTTCTGTTATCCTTACATGT~~CCAATGGC~~
30 AGTGT~~CGCTTCTCGT~~CTCAAAGCTAAACCGGATTGGATTGGGCCACAAAGAAAGCGAATA
GCATTAGGAGCAGGAAGAGGGTTGCTGTATTG~~CATGAGCAATGT~~GATCCAAGATCATT
CACCGT~~GATGT~~CAAAGCTCGAACATACTTCTGACGATTACTTGAAGCTGTTGCGGA
GATTCGGGTTGGCTAAGCTTGGATCATGAGGAGTCGCATGTGACAACCGCCGTGAGA
GGAACAGTGGGT~~CACATTGCAC~~CTGAGTATCTCAACAGGACAATCTCTGAGAAGACA
35 GATGTGTT~~CGGTT~~TCGGATTCTCTCGAATTGATTACTGGATTGAGAGCTCTGAA
TTCGGAAAAGCAGCAAACAAAGAGGGAGCGATACTGATTGGTAAAGAAACTACAACAA
GAGAAGAAGCTAGAACAGATAGTAGACAAGGATTGAAGAGCAACTACGATAGAATAGAA
GTGGAAGAAATGGTTCAAGTGGCTTGT~~ACACAGT~~TATCTCCCATT~~CACCGT~~CCT
AAGATGTCTGAAGTTGTGAGAATGCTGAAGGCGATGGTCTTGTGAGAAATGGGAAGCT
40 TCTTCTCAGAGAGCAGAAACCAATAGAAGTTACAGTAAACCTAACGAGTTTCTCCTCT

GAACGTTATTCGGATCTTACAGATGATTCCCTCGGTGCTGGTTCAAGCCATGGAGTTATCA
GGTCCAAGATGAcaagagaaaactatatgaatggcttgggttgtaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS14 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as 10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain 15 contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to 20 contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine 25 protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein 30 interactions.

MLQGRREAKKSYALFSSTFF

FFFICFLSSSSAELTDKV

35 VALIGIKSSLTDP

HGVLMNWDDTAVD

PCSWNMITCSDGFVIR

LEAPSQNLSGTLSS

SIGNLTNLQTVYRLLQNNYITGNI

PHEIGKLMKLKTLDLSTNNFTGQI

5 PFTLSYSKNLHRRV NNNSLTGTI

PSSLANMTQLTFDLDSYNNLSGPV

PRSLAKTFNVMGNSQICPT

GTEKDCNGTQPKPMISITLNSSQR

10 TKNRK

IAVVFGVSLTCVCLLIIGFGFLLWW

RRRHNKQVLFFDINEQNKE

15 EMCLGNLRRFNFKELQSAT

SNFSSKNLVKGFFGNVYKGCLHD

GSIIAVKRLKDINNGGEVQFQ

TELEMISLAVHRNLLRYGFCT

20 TSSERLLVYPYMSNGSVA

SRLKAKPVLDWGTRKRIALGAG

RGLLYLHEQCDPKIIHRDVKAA

NILLDDYFEAVVGDFGLAKL LD

HEESHVTTAVRGTVGHIAPEYL

25 STGQSSEKTDVFGFGILLLELI

TGLRALEFGKAANQRGAILDW

VKKLQQEKKLEQIVDKDLKS NY

DRIEVEEMVQVALLC TQYLPIH

RPKMSEVV RMLE

30

GDGLVEKWEASSQRAET

NRSYSKPNEFSSS

ERYSDLTDDSSVLVQAMELSGPR

35

Legends

Figure 1

5

The different domains of the predicted RKS gene product have the following functions:

The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in

10 targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein

15 protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation.

The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and

20 Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a single transmembrane

25 domain (<http://genome.cbs.dtu.dk/services/TMHMM/>). At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine

/threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062). The kinase domain is followed by a domain

30 with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

Figure 2

35 Alignment of the predicted protein sequences of the different RKS gene products from *Arabidopsis thaliana* with alignX, Vector NTI Suite 5.5 resulted in a phylogenetic tree in which

the relative homology between the different RKS members is shown.

Figure 3

5 Intron-Exon bounderries of the genomic regions on the chromosomes of *Arabidopsis thaliana* encoding the different RKS gene products. Exons are shown as boxes, whereas intron sequences are shown as lines. Sequences encoding LRR domains are displayed in gray colour, transmembrane regions in black.

10

Figure 4.

Cromosomal location of RKS genes in *Arabidopsis thaliana*, showing colocalisation with GASA genes.

15 Figure 5. A signaling complex comprising molecules of RKS proteins, ELS proteins, NDR/NHL proteins and SBP/SPL proteins.

Figure 6.

Second generation (T2) tobacco seedlings germinated on MS medium. Transformations were performed with DNA clone 2212-15, representing the overexpression construct GT-RKS4-s. T2 seedlings derived from T1 plant 15.7 shows co-suppression effects while T1 plant 15.6 shows no obvious changes in level of RKS4. T1 plants 15.9 and 15.3 show overexpression effects. 25 Plant 15.7 has the lowest remaining level of RKS4 gene product, whereas plant 15.3 has the highest level of RKS4 gene product.

Figure 7

30 Second generation (T2) tobacco plants. In the upper row the offspring from a co-suppressing T1 plant 15.7 is shown. The middle row shows plants derived from a transgenic T1 plant 15.6 with no clear changes in level of RKS4 is shown while the bottom row shows plants derived from a T1 plant 15.3 in which 35 the levels of RKS4 are increased by the introduction of the overexpression construct GT-RKS4-s.

Figure 8

Second generation (T2) tobacco plants. Plants derived from a co-suppressing T1 plant 15.7 show a reduction in plant size and a delay in the initiation and outgrowth of primordia. The 5 control empty vector transgenic plants show no visible differences in growth compared with the offspring from the transgenic 15.6 plant, in which the endogenous level of RKS4 gene product was not changed. In the overexpressing plants 15.9 and 15.3 organ size was increased, similar as the number 10 of initiated leaf primordia.

Figure 9

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (right picture) due to the 15 presence of a transgenic RKS4 antisense construct (GT-RKS4- 16a). The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ 20 primordia is decreased in the transgenic antisense plant compared with the wildtype control.

Figure 10.

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (bottom left picture) due to 25 the presence of a transgenic RKS4 antisense construct (GT- RKS4-16a). The upper right picture shows a wildtype flower of the same age as the transgenic antisense flower, grown under similar growth conditions. Total flower size is only slightly decreased in the transgenic antisense flower compared with the 30 control flower, whereas organ size of petals is strongly decreased.

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is increased (upper left picture) due to the presence of a transgenic RKS4 overexpressing construct 35 (GT-RKS4-6s). Compared with the wildtype control flower, total flower size of the transgenic flower is clearly increased. Both sepal and petal organ size is clearly increased compared

with the control.

For comparison an *Arabidopsis thaliana* WS plant is shown which has been transformed with a construct encoding the GASA3 gene in sense direction, i.e. overexpressing GASA3.

5

Figure 11.

Formation of meristematic regions in the hypocotyl of *Arabidopsis thaliana* WS plants under influence of overexpression of RKS4.

10 RKS4 overexpression results in increases in flower and seed organ size that could be due to increase in cell elongation and/or cell division. In order to analyse the cell division patterns in plants with deregulated RKS4 expression the mitotic activity in transgenic plants was analyzed with the a
15 unstable GUS reporter under the control of a cyclin B1;1 promoter (the Plant Journal 1999 (4) 503-508 Spatio-temporal analysis of mitotic activity with a labile cyclin-GUS fusion protein). *Arabidopsis thaliana* WS seedlings with the pCDG construct did not show gus activity (cell division) in
20 hypocotyls (top) whereas the same pCDG line crossed with a constitutive RKS4 construct showed mitotic activity as indicated by GUS-positive cells (bottom); indicating that RKS4 overexpression activated mitotic activity in hypocotyls.

25 **Figure 12**

In *Arabidopsis thaliana* WS, the seed size is influenced by changing levels of RKS4 gene product. Constitutive overexpression of RKS4 results in increases in seed size (left) compared with control wildtype seeds (right). Antisense
30 constitutive expression of RKS4 cDNA (middle) results in a decrease in seed size compared with the control (right). Magnification is identical in all photos as shown by the bar size.

35

Figure 13

Organ size can be influenced by either modulating cell division or cell elongation or a combination of both. In order to identify the total number of cells and the cell size within an organ the apical site of petals of mature *Arabidopsis* flowers was investigated. Petal organ size is clearly influenced by modulation of RKS4 gene product levels (bottom row for the flowers from which the apical petal epidermal cells were identified). Epidermal cell size is not changed in transgenic plants compared with the control.

10

Figure 14

Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is increased (right picture) due to the presence of a transgenic RKS10 overexpressing construct. The left picture shows the apical epidermus of a full grown cotyl from an empty vector transgenic seedling of the same age as the transgenic overexpressing cotyl, grown under similar growth conditions..

20 Figure 15

Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is decreased (right picture) due to the presence of a RKS10 antisense construct. The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia remains similar in both the transgenic antisense plants and the wildtype control.

30 Figure 16

In order to determine organ size variations in transgenic RKS10 transgenic plants compared with empty vector control transgenic plants (pGreen4K), flower organ size was determined of the four open flower stages of *Arabidopsis* inflorescences. The four successive flower stages are photographed under similar magnifications. No obvious changes in organ length could be observed in size of sepals, petals, stamen and carpel

between empty vector control flowers (pGreen4K), flowers with an antisense RKS10 construct (a) or plants overexpressing the RKS10 cDNA under the control of a 35S promoter (S

5 **Figure 17**

Tissue cultured auxin treated *transgenic Arabidopsis* T2 seedlings were grown on MS agar plates without hormones for a period of 3 weeks. Regeneration potential was scored and the formation and outgrowth of multiple shoot apical meristems from single seedling origin was displayed as (+). The formation and outgrowth of only one shoot apical meristem, leading to the formation of a normal rosette of leaves from individual plants was displayed as (-). Positive regeneration controls consisted of seedlings overexpressing either KNAT1, CUC2, IPT or cycD3. All of these showed an increase of regeneration capacity (+) compared with a negative control GUS overexpressing plant pGreen5K (-). Representative examples of RKS and ELS cDNA overexpressing (s) or antisense (a) cosuppressing constructs in transgenic plants are shown in the bottom panels.

Figure 18.

Tobacco leaf discs were stably transformed with the RKS0 overexpressing construct GT-RKS0-23S and from a single transformation event, large numbers of regeneration plantlets were isolated and subcultured. All of the regenerated plants were potted and flowered. The original transformation event could be kept continuously in tissue culture indefinitely.

30 **Figure 19**

Seedlings from transgenic *Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen5K, overexpressing the GUS gene) in which fasciation could never be observed.

Figure 20 - 23

Primary root tips of transgenic *Arabidopsis* plants (top rows) photographed under similar magnification. The bottom rows show

5 the corresponding seedlings (also between each other under the same magnification). Figure 23 shows the specific *Arabidopsis* transgenes with a strong increase in root outgrowth.

Figure 24

10 Avarage root length of 10-30 transgenic *Arabidopsis* T2 seedlings from one T1 transgenic plant is shown.

Figure 25

15 T3 seedlings are shown from a strong co-suppressing RKS10 antisense construct line (T1-4; T2-6; T3 generation) and a strong overexpressing line (T1-4; T2-6; T3 generation). The overexpressing line is different and stronger from the one shown in Figure 4.1-4.5. Pictures are taken under similar magnifications.

20

Figure 26

T2 seed was germinated on horizontal MS agar plates and pictures were taken under similar magnification of representative examples of the lateral root development from
25 transgenic RKS and ELS transgenic roots.

Figure 27

Pictures taken from transgenic RKS8 or RKS10 overexpressing roots taken directly behind the tip zone. Pictures are taken
30 under same magnification.

Figure 28

Arabidopsis thaliana WS plants in which the endogenous level of RKS or ELS gene product is modified result in the formation
35 of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K).

Overexpression of RKS10 and ELS1 (S) and cosuppression with antisense constructs of RKS8 and also RKS10, result in increased numbers of developing generative meristems. The generative shoots are photographed with similar magnification.

5 magnification.

Figure 29

Arabidopsis thaliana WS plants in which the endogenous level of RKS gene product is modified result in the formation of new 10 meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic Arabidopsis plants compared with control empty vector control plants (pGreen4K). The top panel shows adult plants under similar magnification. Compared with the control, RKS10 overexpression results in an extreme 15 bushy phenotypic plant. The results of co-suppressing the RKS8 gene product are less dramatic with respect to the bushiness. However, also in these transgenic plants the number of 20 generative meristems is strongly increased compared with the control. The bottom panel shows the generative shoot in detail under similar magnification.

Figure 30

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex 25 transgenic flower structure seen in transgenic Arabidopsis plants containing an antisense (a) RKS10 construct. The terminal flower meristem produces 2 sepals, 1 petal, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and 30 stigmatic cells protruding from the top part. Two new flowers are protruding from this structure, containing all flower organs in normal numbers.

Figure 31

35 Schematic drawing of the different flower organs in a complex transgenic flower structure seen in transgenic Arabidopsis plants T1-11 containing an antisense (a) RKS10 construct. The

terminal flower meristem produces 1 sepal, 2 petals, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. An undetermined flower meristem is protruding from the open carpel structure and forms a number of new flowers, including normal flowers (right) and another abnormal flower (left) which consists of a flower with half of the sepal, petal and stamen organs formed and a new terminal flower meristem protruding from this structure, developing in structures as seen in Figure 7.5. The stamen contain only small numbers of (viable) pollen compared with wildtype stamen (see also chapter 5).

Figure 32

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-11 containing an antisense (a) RKS10 construct (overview shown in Figure 7.4). The terminal flower meristem produces half the normal number of sepals, petals and stamen. The remaining part of the flower structure has converted into a new structure containing a new stem containing a single organ structure resembling a fusion between a petal and a sepal. On this structure several (viable) pollen grains can be observed.

Figure 33

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-12 containing an antisense (a) RKS10 construct. The terminal flower meristem originating from an undetermined generative meristem is here producing an axillary secondary undetermined meristem (left picture), a single organ resembling a stamen (bottom left), a normal flower and a terminal flower. This terminal flower structure contains 2 normal sepals, 2 normal petals, 2 normal stamen (with only a few viable pollen) and two organs resembling a fusion of

sepals /petals/stamen (see also figure 7.7). From this terminal flower structure two new flowers emerge (in a similar fashion as observed in Figure 7.3) containing normal numbers of flower organs (right photos). At the top of this figure a 5 control inflorescence is shown schematically with terminal flower meristems as normally originate from the generative *Arabidopsis thaliana* generative meristem.

Figure 34

10 Schematic drawing and detailed pictures of several of the structures as shown in figure 7.6. At the right the organs resembling a fusion between sepals/petals/stamen are shown with viable pollen sticking out from these structures. At the top left the single stamen-like organ directly protruding from 15 the main stem is shown.

Figure 35

Transgenic *Arabidopsis* plants overexpressing the RKS13 gene product show a modification of the normal flower inflorescence 20 architecture, somewhat resembling the structures observed in RKS10 antisense plants. A terminal flower containing a normal seed developing siliques and a small number of sepals, petals and stamen, develops at least 4 additional terminal flower meristems that develop abnormally themselves, resulting in 25 open carpel structures and modifications of organ structures.

Figure 36

Transgenic plants in which the RKS and / or ELS genes are introduced behind a constitutive 35S promoter in an 30 overexpressing (S) or antisense (a) configuration are analyzed for sterility and characterized further for defects in proper pollen development. As a negative control the normal pollen development of a transgene containing the empty expression vector (pG4K) was included. First generation transgenic 35 flowers of RKS10 expressing constructs and second generation control vector and ELS2 are shown under similar magnification. In detail the stigmatic surface and surrounding stamen, are

shown under similar magnification, showing the presence or absence of pollen on the stamen or the stigmatic surface.

Detailed description

1.Modifying organ size

5

Plant size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an

10 increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these

15 processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL

20 protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant 25 growth, proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase:

the size of plant organs

30 the growth rate

the yield of harvested crop

the yield of total plant material

the total plant size

35 Decreasing the levels of endogenous RKS gene product is provided in order to decrease:

the size of plant organs

the growth rate
the total plant size

5

Results obtained (see also figures 6 to 13)

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. The phenotype observed in transgenic plants with antisense constructs of RKS4 (GT-RKS4-a) could be described as dwarf plants in which all plant organs showed a decrease in organs size and growth rate. Overexpression of RKS4 (GT-RKS4-s) resulted in plants with increased size of organs and an increase in growth rate. Since cell size alone was not responsible for the modifications in organ size of petals it can be concluded that RKS4 is involved in the regulation of the cellular divisions during plant growth and organ formation. Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division rates.

25

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2. Cell division

The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent Herewith the invention provides a method for modulating the number of cells to be formed within an eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes, especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

30 Possible Applications

Elevation of the levels of the regulating RKS signaling complex members in plant cells in order to increase:

- the size of plant organs
- the growth rate
- 35 the yield of harvested crop
- the yield of total plant material
- the total plant size

Decreasing the levels of endogenous RKS signaling complex members in order to decrease:
the size of plant organs

- 5 the growth rate
the total plant size

Results obtained

Overexpression and antisense constructs of full length RKS

10 cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.

15 Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division . Another example of RKS genes involved in cellular proliferation is provided by RKS10. Overexpression of RKS10 20 (S) results in a decrease in apical epidermal cells (Figure 14) compared with control plants containing an empty expression cassette (pGreen4K). Co-suppressing the endogenous RKS 10 gene in plants containing an antisense construct (a) showed clearly larger epidermal cells as the corresponding 25 cells in wildtype control plants (Figure 15).. In contrast to the plant phenotypes shown in RKS4 transgenic plants , no differences in plant or organ size could be observed in the RKS10 transgenic plants or organs. This shows that although the organ size remains constant, the number of cells within 30 these organs is variable due to the differences in size of individual cells. These results indicate that normal RKS4 function within the plant can be described as an activator of cellular division.

Normal RKS10 function also involves an activation process on 35 cellular division rate. This effect is also detectable in the root in the region directly behind the tip zone, where in the RKS10 overexpressing transgenes cellular divisions were

detectable in a region where normally cell proliferation has ceased. The plane of divisions of root cells in these transgenes is also clearly different from the normal plane of root cell division, resulting in clumps of cells with all
5 types of division planes possible.

In contrast to RKS4, the final organ size in RKS10 transgenic plants is under the control of other organ size restriction processes, in such a way that the final organ volume remains constant (Figure 16). RKS4 and RKS10 are essentially involved
10 in the same cell cycle activation process, but either addition organ size controlling functions of these RKS genes or the hierarchical order in which they regulate the cell cycle is different.

15

Literature

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3. Regeneration

Modification the levels of different RKS and ELS genes within
5 plants allows the initiation and / or outgrowth of apical
meristems, resulting in the formation of large numbers of
plantlets from a single source. A number of gene products that
is able to increase the regeneration potential of plants is
known already. Examples of these are KNAT1, cycD3, CUC2 and
10 IPT. Here we show that modulation of the endogenous levels of
RKS genes results in the formation of new shoots and plantlets
in different plant species like *Nicotiana tabacum* and
Arabidopsis thaliana. herewith the invention provides a method
15 for modulating a developmental pathway of a plant or plant
cell comprising modifying a gene or modifying expression of
said gene, wherein said gene is encoding a protein belonging
to a signaling complex comprising RKS protein, ELS protein,
NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein,
allowing modulating apical meristem formation, in particular
20 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or
RKS10 gene or functional equivalent thereof. A direct
application of a method according to the invention is the
stable or transient expression of RKS and ELS genes or gene
products in order to initiate vegetative reproduction.
25 Regeneration can be induced after overexpression of for
example RKS0 and ELS1; or by co-suppression of for example the
endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or
co-suppression of these RKS and ELS gene products can be
either transient, or stable by integration of the
30 corresponding expression cassettes in the plant genome.

Results obtained

Overexpression and antisense constructs of full length RKS and
ELS cDNA clones have been made under the control of 35S
35 promoters. Transgenic plants have been produced in *Arabidopsis*
thaliana and in *Nicotiana tabacum*. Subsequent generations of

stably transformed plants were investigated for phenotypes and analyzed in detail.

T2 transgenic seedlings of *Arabidopsis* were germinated in liquid MS medium supplemented with 1 mg/L 2,4-D for 1 week, followed by extensive washing and plating of the seedlings onto MS agar plates without hormones. Control transgenic seedstocks containing either a negative control vector (pGreen5K); or positive control overexpression constructs of gene products known to increase the regeneration potential (IPT, KNAT1, CUC2 and cycD3) were characterized for regeneration potential together with seedstocks from plants either overexpressing (s) or co-suppressing (a) all RKS and ELS gene products (Figure 17). Overexpression of the ELS1 and RKS0 cDNA clones resulted in an increase of shoot apical meristem formation and outgrowth, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only increased regeneration results are shown). Antisense constructs of RKS3, RKS4, RKS8 and RKS10 also resulted in an increased formation and outgrowth of apical meristems (Figure 17).

T1 generation *Nicotiana tabacum* tissue cultures transformed with ELS and RKS gene products in either overexpression (s) cassettes or antisense co-suppression (a) cassettes allowed the regeneration of indefinite number of offspring plants from a single transformed cell origin (Figure 18). An example is shown for the overexpression of the GT-RKS0-23S construct. The resulting plants obtained from one transformation event in general showed no phenotypes. Only a subset of plants displayed RKS0 overexpression phenotypes (like loss of apical dominance and early flowering).

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4. Fasciation

Fasciation is normally a result from an increased size of the
5 apical meristem in apical plant organs.

Modulation of the number of cells within the proliferating
zone of the shoot apical meristem results in an excess number
of cellular divisions, giving rise to excess numbers of
primordia formed or to stems in which the number of cells is
10 increased. The invention herewith provides a method for
modulating a developmental pathway of a plant or plant cell
comprising modifying a gene or modifying expression of said
gene, wherein said gene is encoding a protein belonging to a
signaling complex comprising RKS protein, ELS protein, NDR/NHL
15 protein, SBP/SPL protein and RKS/ELS ligand protein allowing
modulating fasciation, in particular wherein said gene
comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional
equivalent thereof. Here we for example show that modulation
of the levels of RKS gene products in plants like *Arabidopsis*
20 *thaliana* can result in fasciated stems as shown in Figure 19.
A direct application as provided herein is the regulated
formation of fasciation in plant species in which such a trait
is desired like ornamental plants. Regulation of the
initiation and extent of fasciation, either by placing the
25 responsible RKS encoding DNA sequences under the control of
stage or tissue specific promoters, constitutive promoters or
inducible promoters results in plants with localized or
constitutive fasciation of stem tissue. Another application is
modulating the number of primordiae by regulation of the
30 process of fasciation. An example is provided by for example
sprouts, in which an increased number of primordia will result
in an increased numbers of sprouts to be harvested. Fasciation
can also result in a strong modification in the structural
architecture of the inflorescence, resulting in a terminal
35 group of flowers resembling the *Umbelliferae* type (an example
is shown in Figure 19 where the fasciated meristem of a RKS0-
7S *Arabidopsis* plant in which endogenous RKS0 gene product

levels have been deregulated clearly terminates in an *Umbelliferae* type inflorescence.

Results obtained

- 5 Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
- 10 T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector (pGreen5K) were tested for their ability to induce fasciation (Overexpression constructs (s) of RKS0, RKS8 and RKS10 cDNA clones resulted in 15 fasciated plants, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only positive results are shown). Antisense constructs of RKS3 gave also rise to fasciation (Figure 19).

20

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5. Root development

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the 5 number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased.

Adaptation to soil conditions is possible by regulation of 10 root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of the RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene 15 or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular wherein said gene comprises an ELS1, ELS2, RKS1, 20 RKS3, RKS4, RKS6 RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length 25 can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products.

Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co- 30 suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by

35 overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant

hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.

T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector pGreen4K (empty expression vector) and / or pGreen5K (a GUS overproducing vector) were included as references for normal root development. Seedlings from transgenic *Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen4K, containing an expressing cassette without an insert cDNA). Seedlings are germinated and grown on vertically placed MS agar plates.

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Cell 3: 1147-1154

6. Apical meristems

All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering.

Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows

the formation of completely new types of flowers and fused fruit structures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression 5 results in an extremely bushy phenotype.

Results obtained

Changing the normal levels of endogenous RKS10 within the 10 plant, either by overexpressing or co-suppressing the RKS10 cDNA, results in an increase in generative meristem development (Figure 28).

Compared with the control empty vector transgenic pGreen4K plants, large number of meristems are initiated at places were 15 normally no meristems initiate and / or develop. A clear example is shown by co-suppressing the RKS8 gene (Figure 29), where many new inflorescence meristems are initiated from the central generative meristem compared with control pGreen4K plants of the same age. This phenotype is even more extreme in 20 RKS10 overexpressing plants where the resulting plants are extremely bushy with very large numbers of generative meristems formed. Inactivation of the endogenous RKS10 gene in *Arabidopsis* results in modification of meristematic identity as can be shown in Figure 30. A determined flower meristem 25 develops into two new normal terminal flower meristems and a number of terminal flower organ primordia. Another example is shown in Figure 31 where meristem determination is switched from a terminal flower meristem, that normally result only in the normal numbers of terminal organ primordia, towards a 30 number of organ primordia, a new undetermined generative meristem that develop into normal flowers or in a new terminal flower meristem with developmental abnormalities. Only half of the terminal flower primordia develop normally while an extra structure arises resembling a new flower stem with a 35 petal/stamen like organ. The few pollen detectable on this structure (Figure 32) were able to pollinate a MS1 (male sterile) *Arabidopsis* flower. Figure 33 shows the meristematic

developmental switch from a terminal flower meristem into a new undetermined generative meristem, that gives rise to a new formation of another undetermined meristem, and several normal and abnormal terminal flowers. The abnormal flowers again show
5 the fusion of different structures, in this case from sepals, petals and stamen together (Figure 34). Surprisingly, directly on the generative stem another structure, resembling a single stamen was detectable. All these data indicate that a decrease in RKS1 expression levels results in switches in the
10 meristematic identity. Meristems can switch forward and backward between developmental stages, indicating that RKS10 is normally involved in regulating the meristematic identity and the developmental order of meristematic development. RKS13 seems to be involved in similar processes, as can be concluded
15 from the switches in flower meristematic outgrowths observed in figure 35. Modification of the expression levels of RKS1 also results in modified meristem identity. Suppression of endogenous RKS1 levels results in a developmental switching of generative meristems towards vegetative meristems, together
20 with other phenotypes (results not shown).

Literature

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7. Male sterility

Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired.

Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, Agrobacterium transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

30 **Results obtained**

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic plants

containing a negative control vector pGreen4K (empty expression vector) were included as references for normal stamen and pollen development. RKS10 and ELS2 resulted in sterile plants when overexpressed in *Arabidopsis*. Antisense 5 RKS10 plants resulted in a strong reduction in the number of pollen formed (Figure 36). In order to determine whether pollen development itself was the reason for sterility (and not a combination of pollen developmental mutants coupled to either embryo lethals or female gametogenesis defects), 10 reciprocal crosses were performed between sterile transgenic plants and wildtype *Arabidopsis thaliana* WS plants. These results confirmed that the sterile plants with overexpressing RKS10 and ELS2 constructs were male sterile but completely female fertile. No defects could be observed in embryo 15 development from crosses between female transgenic overexpressors and male wildtype pollen (results not shown). Since both antisense and overexpressing constructs of the RKS10 gene showed defects in proper pollen development we conclude that normal levels of endogenous RKS10 gene product 20 are essential for proper pollen formation, outgrowth and differentiation. In the ELS2 overexpressing plants the initiation of pollen grains was not inhibited. However the proper development of pollen grains in full grown viable pollen was clearly inhibited .

25

Literature

- The *Arabidopsis* male sterility1 (MS1) gene is a transcriptional regulator of male gametogenesis, with homology 30 to the PHD-finger family of transcription factors. Wilson et al. 2001. the Plant Journal 28: 27-39
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8. Resistance mechanisms

Two-hybrid interaction experiments have already shown *in vitro* interaction between RKS and NDR0-NHL and members of the SBP/SPL family. Here we show that *in vivo* the individual components of this signalling cascade are regulating identical processes, as based on functional genomics on transgenics plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex.

Here we show a large number of new members of the NDR/NHL gene family and we postulate a function as syntaxins in the pathogen resistance:

15 **At2g27080;**

MAERVYPADS PPQSGQFSGN FSSGEFPKKP APPPSTYVIQ VPKDQIYRIP PPENAHRF EQ
LSRKKTNRSN CRCCFCFSFLA AVFILIVLAG ISFAVLYLIY RPEAPKYSIE GFSVSGINLN
STSPISPSFN VTVRSRNGNG KIGVYYEKES SVDVYYNDVD ISNGVMPVFY QPAKNVTVVK
LVLSGSKIQL TSGMRKEMRN EVSKKTVPFK LKIKAPVKIK FGSVKTWTMI VNVDCCDVTVD
20 KLTAPSRIVS RKCSHDVDLW **

At5g21130

MTVEKPQEML GDTNSDGFLT NKDVHRIKHP SLDTNDSSSS RYSVDSQKSR IGGPPGTYVI
KLPKDQIYRV PPPENAHRYE YLSRRKTNKS
25 CCRRCCLCYSL SALLIIIVLA AIAFGFFYLV
YQPHKPQFSV SGVSVTGINL TSSSPFSPVI RIKLRSQNVK GKLGЛИYEKG NEADVFFNGT
KLGNGEFTAF KQPAGNVTVI VTVLKGSSVK LKSSSRKELT ESQKKGVPF GLRIKAPVKF
KVGSVTTWMT TITVDCKITV DKLTASATVK TENCETGLSL L*

30 **At1g65690**

MSQHQKIQPV QDPEAATARP TAPLVPRGSS RSEHGDPSKV PLNQRPQRFV PLAPPKKRRS
CCCRCFCYTF CFLLLLVVAV GASIGILYLV FKPKLPDYSI DRLQLTRFAL NQDSSLTTAF
NVTITAKNPN EKIGIYYEDG SKITWYMEH QLSNGSLPKF YQGHENTTVI YVEMTGQTQN
35 ASGLRTTLEE QQRTGNIPL RIRVNQPVRV KFGKLKLFEV RFLVRCGVFV DSLATNNVIK
IQSSSCKFRL RL*

At5g36970

MSDHQKIHIV SDPEAPPHT APLVPRGSSR SEHGDPTKTQ QAAPLDPPRE KKGSRS
CWCRVCYCPLLVLF LLIVIVGAIV GILYLFRPK FPDYNIDRLQ LTRFQLNQDL
40 SLSTAFNVTI
TAKNPNEKIG IYYEDGSKIS VLYMQTRISN GSLPKFYQGH ENTTIILVEM TGFTQNATSL
MTTLQEQQRL TGSIPLRIRV TQPVRIKLGK LKLMKVRFLV RCGVSVDLSA ANSVIRVRSS
NCKYRFRL*

45 **At1g54540**

MGDQQKIHIV LQMEANKTKT TTPAPGKTVL LPVQRPIPPP VIPSKNRNMC CKIFCWVLSL
LVIALIALAI AVAVVYFVFH PKLPSYEVNS LRVTNLGINL DLSSAEFKV EITARNPNEK
IGIYYEKGGH IGVWYDKTKL CEGPIPRFYQ GHRNVTKLNV ALTGRAQYGN TVLAALQQQQ
50 QTGRVPLDLK VNAPVAIKLG NLKMKKIRIL GSCKLVDSDL STNNNNNIKA SDCSFKAKL*

At5g06320

MADLNGAYYG PSIPPPKKVS HSHGRRGGC GCLGDCLGCC GCCILSVIFN ILITIAVLLG
 IAALIIWLIF RPNAIKFHVT DAKLTEFTLD PTNNLRYNLD LNFTIRNPNR RIGVYYDEIE
 VRGYYGDQRF GMSNNISKFY QGHKNTTVVG TKLVGQQLVL LDGGERKDLN EDVNSQIYRI
 DAKLRLKIRF KFGLIKSWRF KPKIKCDLKV PLTSNSTSGF VFQPTKCDVD F**

5

At5g11890

MTDRVFPASK PPTATNGAPP VGSIPPPPAP ATVTSNGTTN GMANQKPQVY IPANRPVYRP
 QPYSSRRHHQ SRPSCRRICC CCCFWSILII LILALMTAIA ATAMYVIYHP RPPSFVPSI
 RISRVNLITS SDSVSHLSS FFNFTLISEN PNQHLSFSYD PFTVTVNSAK SGTMGLNGTV
 PAFFSDNGNK TSFHGVIATS TAARELDPDE AKHLRSDLTR ARVGYEIEMR TKVKMIMGKL
 KSEGVEIKVT CEGFEGTIPK GKTPIVATSK KTKCKSDLSV KVWKWSF*

10

At1g17620

MTDDRVYPAS KPPAIVGGGA PTTNPTFPAN KAQLYNANRP AYRPPAGRRR TSHTRG
 CCCRCCCWTIFVII LLLLIVAAAS AVVYLIYRPQ RPSFTVSELK ISTLNFTSAV
 RLTTAISLSV
 IARNPNKNVG FIYDVTDTIL YKASTGGDDD VVIGKGTIAA FSHGKKNTTT LRSTIGSPPD
 ELDEISAGKL KGDLKAKKAV AIKIVLNSKV KVKGALKTP KSGIRVTCEG IKVVAPTGKK
 ATTATTSAAK CKVDPRFKIW KITF**

20

At3g11650

MGSKQPYLNQ AYYGPSIPPP PKAHRSYNSP GFGCCCFSCl GSCLRCCGCC ILSLICNILI
 AVAVILGVAA LILWLIFRPN AVKFYVADAN LNRFSFDPPN NLHYSLDLNF TIRNPNQRVG
 VYYDEFSVSG YYGDQRFGSA NVSSFYQGHK NTTVILTKIE QONLVVLDG ARTDLKDEK
 SGIYRINAKL RLSVRFKFWF IKSWKLKPQI KCDDLKIPLG SSNSTGGFKF QPVQCDFDLS**

At2g22180

MEGPRRPPSA TAPDSDDDQP DDPPSVWHRP TSSLPALPSL DPPSHGSHHW RNHSLNLSPL
 PTTSSPPLPP PDSIPELETY VVQVPRDQVY WTPPPEHAKY VEKRSKNPEK NKKKGCSKRL
 LWFFIILVIF GFLLGAIILLI LHFAFNPTLP VFAVERLTNV PSNFETVLRA ENPTSNMGVR
 YMMEKNGVVS LTYKNKSLGS GKFPGLSQAA SGSDKVNVL NGSTKNAVQQ PRGSKQPVVL
 MLNMELKAES EAGPVKRNE VVTCVDVKVK GLLDACKVEI VSENCESEFK N*

35

At5g22870

MCHKPKELEM PMETSPAQPL RRPSLICYIF LVILTLIFMA AVGFLITWLE TKPKKLRYTV
 ENASVQNFNL TNDNHMSATF QFTIQSHNPN HRISVYYSSV EIFVFKFDQT LAFDTVEPFH
 QPRMVVKQID ETLIAENVAV SKSNGKDLRS QNSLGKIGFE VFVKARVRFK VGIWKSSHRT
 AKIKCSHVTV SLSQPNKSQN SSCDADI*

40

At2g35980

MAAEQPLNGA FYGPSVPPPA PKGYYRRGHG RGCGCCLLSL FVKVIISLIV ILGVAALIFW
 LIVRPRAIKF HVTDASLTF DHTSPDNILR YNLALTVPVR NPNKRIGLYY DRIEAHAYYE
 GKRFSTITLT PFYQGHKNTT VLTPTFQGQN LVIFNAGQSR TLNAERISGV YNIEIKFRLR
 VRFKLGDLKF RRIKPKVDCD DLRLPLSTSN GTTTSTVFP IKCDFDF**

45

At2g46300

MADYQMNVPVQ QKPPGYRDPM MSSPPPPPPP IQQQPMRKAV PMPTSYPK KRRSCCRFCC
 CCICITLVLF IFLLLVGTAV FYLWFDPKLP TFSLASFRLD GFKLADDPDG ASLSATAVAR
 VEMKNPNSKL VFYYGNTAVD LSVGSGNDET GMGETTMNGF RQGPKNSTSV KVETTVKNQL
 VERGLAKRLA AKFQS金陵 NVVAKTKVGL GVGGIKIGML AVNLRCGGVS LNKLTDSPK
 CILNTLKWKYK IISN*

50

At4g05220

MTPDRTTIPI RTSPVPRAQP MKRHHSASYY AHRVRESLST RISKFICAMF
 LLVLFFVGVI AFILWLSLRP HPRPRFHIQDF

55

VVQGLDQPTG VENARIAFNV TILNPNQHMG VYFDSEMEGSI YYKDQRVGLI
 PLLNPFFQQP TNTTIVTGL TGASLTVNSN RWTEFSNDRA QGTVGFRLDI
 VSTIRFKLHR WISKHHRMHA NCNIVVGRDG LILPKFNHKR CPVYFT*

5 At2g35460
 MANGLNGASY GPPIKPPVKT YYSHGRRGSD VGCGICGCFS SCLLCGGCL VNIICNILIG
 VLVCLGVVAL ILWFILRPNV VKFQVTEADL TRFEFDPRSH NLHYNISLNF SIRNPNQRLG
 IHYDQLEVRG YYGDQRFSA NMNTSFYQGHK NTTVVGTELN GQKLVLLGAG GRRDFREDRR
 SGVYRIDVKL RFKLRFKFGF LNSWAVRPKI KCHLKVLST SSSDERFQFH PTKCHVDL*

10 At2g27260
 MQDPSRPATG YPYPPYPNP QQQQPPPTNGY PNPAAGTAYP YQNHNPYYAP QPNPRAVIIR
 RLFIVFTFL LLLGLLFIF FLIVRPQLPD VNLSLSVSN FNVSNNQVSG KWDLQLQFRN
 15 PNSKMSLHYE TALCAMYYNR VSLSETRLQP FDQGKKDQTV VNATLSVSGT YVDGRLVDSI
 GKERSVKGNV EFDLRMISYV TFRYGAFRRR RYVTVYCDDV AVGVPVSSGE GKMVGSSKRC
 KTY**

At4g01410
 MGEGEAKAEH AAKADHKNAP SASSTPESYS KEGGGGGGDA RRAICGAIFT ILVILGIIAL
 20 ILWLVYRPHK PRLTVVGAII YDLNFTAPPL ISTSVQFSVL ARNPNRRVSI HYDKLSMYVT
 YKDQIITPPL PLPPLRLGHK STVVIAPVMG GNGIPVSPEV ANGLKNEAY GVVLMRVVIF
 GRLRWKAGAI KTGRYGFYAR CDVWLRFNPS SNGQVPLLAP STCKVDV*

At5g22200
 25 MTGRYCDQHN GYEERRMRMM MRRIAWACLG LIVAVAFVVF LVWAILHPHG PRFVLQDVTI
 NDFNVSQPNF LSSNLQVTVS SRNPNDKIGI FYDRLDIYVT YRNQEVTLAR LLPSTYQGHL
 EVTVWSFPLI GSAPVAPYL SSALNEDLFA GLVLLNIKID GWVRWKVGSW VSGSYRLHV
 CPAFITVTGK LTGTGPAlKY QLVQRCAVDV *

30 At1g61760
 MHNKVDSLKV RSNPSTRPIS RHHSASNIVH RVKESLTTRV SKLICAIFLS LLLCLGIITF
 ILWISLQPHR PRVHIRGFSI SGSLRPDGFE TSHISFKITA HNPQNQVGIY YDSMEGSVYY
 KEKRIGSTKL TNPFYQDPKN TSSIDGALSR PAMAVNKDRW MEMERDRNQG KIMFRLKVRS
 MIRFKVYTWH SKSHKMYASC YIEIGWDGML LSATKDKRCP VYFT*

35 At3g52470
 MSKDCGNHGG GKEVVVRKLC AIIIAFIVIV LITIFLVWVI LRPTKPRFVL QDATVYAFNL
 SQPNLLTSNF QVTIASRNPN SKIGIYYDRL HVYATYMNQQ ITLRTAIPPT YQGHKEVN
 40 SPFVYGTAVP IAPYNSVALG EEKDRGFVGL MIRADGTVRW KVRLTITGKY HIHRCQAFI
 NLGNKAAGVL VGDNAVKYTL ANKCSVNV**

At5g53730
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 45 YQSHEEINLL TAFLQGTELP VAQSFQYQIS RERSTGKIII GMKMDGKLRW KIGTWVSGAY
 RFNVNCLAIV AFGMNMTTPP LASLQGTRCS TTI*

At4g01110
 50 MAGETLLKPV LQKPPGYREL HSQPQTPLGS SSSSSMLRR PPKHAIPAAF YPTKKRQWSR
 CRVFCCCVCI TVAIVILLI LTVSVFFLYY SPRLPVVRSL SFRVSNFNFS GKGAGDGLSQ
 LTAEATARLD FRNPNGKLRY YYGNVDVAVS VGEDDFETSL GSTKVGFVE KPGNRTVVIV
 PIKVKKQQVD DPTVKRLRAD MKSKKLVVKV MAKTKVGLGV GRRKIVTVGV TISCGGVRLQ
 TLDSKMSKCT IKMLKWyVPI QVKCI*

55 At2g35960
 MTTKDCGNHG GGGGGGTASR ICGVIIGFII IVLITIFLVW IILQPTKPRF ILQDATVYAF

NLSQPNLLTS NFQITIASRN RNSRIGIYYD RLHVYATYRN QQITLRTAIP PTYQGHKEDN
VWSPFVYGN S VPIAPFNAVA LGDEQNRFV TLIIRADGRV RWKVGLTIG KYHLHVRCA
FINLADKAAG VHVGNAVKY MLINKCSVNV *

5 At3g52460
MPSPPEEETQ PKPDTGPGQN SERDINQPPP PPPQSQPPP QTQQQTYPPV MGYPGYHQPP
PPYPNYPNAP YQQYPYAQAP PASYYGSSYP AQQNPVYQRP ASSGFVRGIF TGLIVLVLL
CISTTITWLW LRPQIPLFSV NNFSVSNFNV TGPVFSAQWT ANLTIENQNT KLKGYFDRIQ
GLVYHQNAV EDEFFLATAFF QPVFVETKKS VVIGETLTAG DKEQPKVPSW VVDEMKKERE
10 TGTVTFSLRM AVWVTFKTDG WAARESGLKV FCGKLKVGF E GISGNGAVLL PKPLPCVVY*

At4g09590
MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV WIILQPKNPE FILQDTTVYA
FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQITLASDL PPTYQRHKED
15 SVWSPLLGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGQ VRWKVGLTLI GNYHLHVRCA
AFINQADKAA GVHVGENTVK YTLINKCSVN F*

At2g35970
MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV SIILQPKKPE FILQDTTVYA
20 FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQITLASDL PPTYQRHKEN
SVWSPLLGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGR VRWKVGLTLI GNYHLHVRCA
AFINQADKAA GVHVGENTVK YTLINKCSVN F*

At3g26350
25 MSHHHHHETN PHFARIPSQN PHLKSGGAST SQTSSNQPHI PPIPHPKKSH HKTTQPHPVA
PPGILIKTRG RHRENPIQEP KHSVIPVPLS PEERLPPRKT QNSSKRPLLL SPEDNQQQRP
PPPQAPQRNG GGYGSTLPPI PKPSPWRATP TPSPHRRGP RLPPPSRETN AMTWSAAFCC
AIFWVILILG GLIILIVYLV YRPRSPYVDI SAANLNAAYL DMGFILLNGDL TILANVTNPS
30 KKSSVEFSYV TFELYYYNTL IATQYIEPFK VPKKTSMFAN VHLVSSQVQL QATQSRELQR
QIETGPVLLN LRGMFHARSH IGPLFRYSYK LHTHCSVSLN GPPLGAMRAR RCNTKR*

At3g11660
MKDCENHGH S RRKLIRRIFW SIIFVLIFI LTILLIWAIL QPSKPRFILQ DATVYAFNVS
GNPPNLLTSN FQITLSSRNP NNKIGIYYDR LDVYATYRSQ QITFPTSIPP TYQGHKDVDI
35 WSPFVYGT S PIAPFNGVSL DTDKDNGVVL LIIRADGRVR WKVGTFITGK YHLHVKCPAY
INFGNKANGV IVGDNAVKYT FTTSCSVSV**

At3g44220
40 MTEKECEHHH DEDEKMRKRI GALVLGFLAA VLFWVFLVWA ILHPHGPRFV
LQDATIYAFN VSQPNYLTSN LQVTLSSRNP NDKIGIFYDR LDIYASYRNQ
QVTLATLLPA TYQGHLDVTI WSPFLYGTTV PVAPYFSPAL SQDLTAGMVL
LNIKIDGWVR WKVGTWVSGR YRLHVNCPAY ITLAGHFSGD GPAVKYQLVQ RCAVDV*

At1g08160
45 MVPPNPAHQ P ARRTQPQLQP QSQPRAQPLP GRRMNPVLCI IVALVLLGLL VGLAILITYL
TLRPKRLIYT VEAASVQEFA IGNNDHINA KFSYVIKSYN PEKHVSRYH SMRISTAHHN
QSVAHKNISP FKQRPKNETR IETQLVSHNV ALSKFNARDL RAEKSKGTIE MEVYITARVS
YKTWIFRSRR RTLKAVCTPV MINVTSSSLD GFQRVLCKTR L**

50 At2g01080
MPPPPSSSRA GLNGDPIAAQ NQQPYYRSYS SSSSASLKGC CCCLFLLFAF LALLVLA
IVILAVKP KK PQFDLQQVAV VYMGISNPSA VLDPTTASLS LTIRMLFTAV NPNKVGIRYG
ESSFTVMYKG MPLGRATVPG FYQDAHSTKN VEATISVDRV NLMQAHAADL VRDASLNDRV
ELTVRGDVGA KIRVMNFDSP GVQVLLPSFL PAFCSLSDL A *

55 At5g06330

MTSKDCGSHD SHSSCNRKIV IWTISIILLL ILVVILLVWA ILQPSKPRFV LQDATVFNFN
 VSGNPPNLNT SNFQFTLSSR NPNDKIGIYY DRLDVYASRY SQQITLPSPM LTTYQGHKEV
 NVWSPFVGYY SVPVAPYNAF YLDQDHSSGA IMMLMLHLDGR VRWKVGFSIT GKYLHVRCH
 ALINFGSSAA GVIVGKYMLT ETCSVSV*

5

At5g56050

MSKFSPPPQS QPQPETPPW ETPSSKWYSP IYTPWRTTPR STQSTPTTTP IALTEVIVSK
 SPLSNQKSPA TPKLDSMEAHL PLHETMVLLQ LRTSRTNPWI WCGAALCFIF SILLIVFGIA
 TLILYLAVKP RTPVFDISNA KLNTILFESP VYFNGDMLLQ LNFTINPNKKL NVRFENLMVE
 10 LWFADTKIAT QGVLPFSQRN GKTRLEPIRL ISNLVFLPVN HILELRRQVT SNRIAYEIRS
 NFRVKAIFGM IHYSYMLHGI CQLQLSSPPA GGLVYRNCTT KRW*

At3g20600**NDR1**

15 MNNQNEDTEG GRNCCTCCCLS FIFTAGLTSF FLWLSLRADK PKCSIQNFFI PALGKDPSR
 DNNTLNFMVR CDNPNKDKGI YYDDVHLNFS TINTTKINSS ALVLVGNYTV PKFYQGHKKK
 AKKWGQVKPL NNQTVLRAVL PNGSAVFRLD LKTQVRFKIV FWKTKRYGVE VGADVEVNGD
 GVKAQKKGIK MKKSDSSFPL RSSFPISVLM NLLVFFAIR*

20 **At3g54200**

MSDFSIKPDD KKEEEKPATA MLPPPKNAS SMETQSANTG TAKKLRRKRN CKICICFTIL
 LILLIAIVIV ILAFTLFKPK RPTTTIDSVT VRDLQASVNP LLLKVLLNLT LNVDSLKNP
 NRIGFSYDSS SALLNYRGQV IGEAPLPANR IAARKTVPLN ITLTLMAIDL LSETQLLSDV
 MAGVIPLNTF VKVTGKVTVL KIFKIKVQSS SSCDLSISVS DRNVTSQHCK YSTKL*

25

At3g20590

non-race specific disease resistance protein, putative
 MTKIDPEEL GRKCCTCFFK FIFTTRLGAL ILWLSLRACK PKCSIQNFYI PALSKNLSSR
 DNNTLNFMVR CDNPNKDKGI YYDDVHLTFS TINTTTTNSS DLVLVANYTV PKFYQGHKKK
 30 AKKWGQVWPL NNQTVLRAVL PNGSAVFRLD LKTHVRFKIV FWKTWYRRI KVGADVEVNG
 DGVKFAQKKGS KTKKSDSSLR LRSSFPIFVLM MNLLVFFAIR *

At4g39740

MSHTATSLA RFTKPVPKPA SSPIVNTKLT TSGGRTAAM DLSSFRRLTVW
 35 DPDTANDSSG KFPWPRFLFF FLTLKTGGSG LNIKPTISAI AQMMNPMTIT
 EMNNQMHRLE QKLLLFLPGS LFLRLSTILH YPGEGRNRPD PLEHALRRSR
 SLGLDQEAAA KKIRVGRDS KNDYVNVEN QAASFLRRCG PSKRIQSVNY
 CKSTRQGHEI PDVKPLFPTG GGTQAPSRSR ARYAVPAILL GFAGFVGFLH
 YNDERRAVPR GQASSNSGCG CGSNTTVKGP IIIGGPFTLVS TENKIVTEND
 40 FCGKWVLLYF GYSFSPDVGP EQLKMMSKAV DKLAILLNPL TFGCLLYAE
 FDSRILGLTG TASAMRQMAQ EYRVYFKKQ EDGEDYLVDT SHNMYLINPK
 MEIVRCFGVE YNPDELSQEL LKEVASVSQ*

At1g32270 syntaxin, putative

45 MVRSDVKFQ VYDAELTHFD LESNNLQYS LSLNLSIRNS KSSIGIHYDR
 FEATVYYMNQ RLGAVPMPLF YLGSKNTMLL RALFEGQTLV LLKGNERKKF
 EDDQKTVYR IDVKLSINFR VMVLHLVTWP MKPVVRCHLK IPLALGSSNS
 TGGHKMILLI GQLVKDTSAN LREASETDHR RDVAQSKKIA DAKLAKDFEA
 ALKEFQKAQH ITVERETSYI PFDPKGFSSE SDVIDGYDRS QEQRVLMESR
 50 RQEIVLLDNE ISLNEARIEA REQGIQEVKH QISEVMEMFK DLAVMVVDHQG
 TIDDIDEKID NLRSAAAQGK SHLVKASNTQ GSNSSLLFSC SLLLFFFSLSG
 DLCRCVCVGS ENPRLNPTRR KAWCEEEDEE QRKKQQKKKT MSEKRRREEK
 KVNPNGFVF CVLGHK*

55 **At1g13050**

MSHHHYETNP HFVQFSLQDQ HQGGPSSWN SPHHHQIPQA HSVAPPRVKI KTRGRHQTEP
 PETIHEPSS RPLPLRPEEP LPPRHNPNSA RPLQLSPEEQ RPPHRGYGSE PTPWRRAPTR
 PAYQQGPKRT KPMTLPATC CAILLIVLIL SGLLLLLVYL ANRPRSPYFD ISAATLNtan
 5 LDMGYVLNGD LAVVVNFTNP SKKSSVDFSY VMFELYFYNT LIATEHIEPF IVPKGMSMFT
 SFHLVSSQVQ IQMIQSQDLQ LQLGTGPVLL NLRGTFHARS NLGSLMRYSY WLHTQCSISL
 NTPPAGTMRA RRCNTKR*

At5g45320

10 MPRLTSRHGT SPFIWCAAII CAIISIVVIV GGIIVFVGYL VIHPRVPIIS
 VADAHLDFLK YDIVGVLQTQ LTIVIRVEND NAKAHALFDE TEFKLSYEGK
 PIAILKAPEF EVVKEKSMFL PYLVQSYPPIP LNPTMMQAVD YAVKKDVITF
 ELKGGSRTRW RVGPLGSVVF ECNLSCQLRF RPSDHSYIPS PCTSAHKH*

At3g20610

15 MDRDDAAWEWF VTIVGSIIMTL LYVSFLLALC LWLSTLVHHI PRCSIHYFYI PALNKSЛИSS
 DNTTLNFMVR LKNINAKQGI YYEDLHLSFS TRINNSSLV ANYTVPRFYQ GHEKKAKKWG
 QALPFNNQTV IQAVLPNGSA IFRVDLKMQV KYKVMWSKTK RYKLKASVNL EVNEDGATKV
 KDKEDGIKMK ISDSSPQRLT FFQVCFSIIC VLMNWLFILA IR*

At4g26490

20 MVLTKPATVR FNGLDAEPRK DRVILRQPRS SRTSLWIWCV AVFLAIRPRI PVFDIPNANL
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 TRLEPIRLIS SLVGLPVNHA VELRRQLENN KIEYEIRGTF KVKAHFGMIH YSYQLHGRCQ
 LQMTGPPTGI LISRNCTTKK *

At5g42860

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 LTSPMGSPPH SHSSSSRFSK INGSKRKGHGA GEKQFAMIEE EGLLDDGDRE
 QEAALPRRCYV LAFIVGFSLL FAFDSLILYA AAKPQPKPKIS VKSITFEQLK
 30 VQAGQDAGGI GTDMITMNAT LRMLYRNTGT FFGVHVTSSP IDLSFSQITI
 GSGSIKKFYQ SRKSQRTVVV NVLGDKIPLY GSGSTLVPPP PPAPIPKPKK
 KKGPIVIVEP PAPPAPVPMR LNFTVRSRAY VLGKLVQPKF YKRIVCLINF
 EHKKLSKHIP ITNNCTVTI *

At1g45688

35 MHAKTDSEVT SLAASSPARS PRRPVYYVQS PSRDSDHDGEK TATSFHSTPV LSPMGSPPHS
 HSSMGRHSRE SSSSRFSGSL KPGSRKVNPN DGSKRKGHGG EKQWKECAVI EEEGLLDDGD
 RDGGVPRRCY VLAFIVGFFI LFGFFSLILYA GAAKPMKPKI TVKSITFETL KIQAGQDAGG
 40 VGTDMITMNA TLRMLYRNTG TFFGVHVTST PIDLSFSQIK IGSGSVKKFY QGRKSERTVL
 VHViGEKIPL YGSGSTLLPP APPAPLPKPK KKKGAPVPIP DPPAPPAPVP MTLSFVVRSR
 AYVLGKLVQP KFYKKIECDI NFEHKNLNKH IVITKNCTVT TV*

At4g26820

45 MDDEQNLVEE MNQOLLITVI DTEKVPELRP ISSRSHQESE PANISHWSLL FKLFЛАITIM
 GACVAGVTBV ILITPTPPTV HVQSMHISFA NHNLPVWSAT FSINKPNEKL HVTYENPSVW
 LVHRGKLVST ARADSFWQKG GEKNEVIVKR NETKVIDEEA AWEMEDEVAV TGGVVGLDMV
 FSGRVGFYPG TSALWGEQYM SAVCENVSAK LYNVDDEIYG TNRSVLSFDG RLVCSVRLPK
 YP*

response, that results in inhibition of the pathogen. After the recognition, further processes appear to be non-specific.

In addition to the hypersensitive response, a second line of defence, defined as the systemic acquired resistance response

5 can be triggered, that renders unaffected parts of the plant resistant to a variety of normally virulent pathogens. Several of the RKS and ELS gene products prove to be key regulators in the regulation of the system acquired resistance response.

10 Overexpression of several of the RKS and / or ELS genes in plants, either by constitutive promoters, stage and / or tissue specific promoters, or inducible promoters allows the activation of a systemic acquired resistance response in plants.

15 Another application can be provided by the activation of a RKS /ELS specific ligand in (transgenic) plants, thereby activating the receptor complex, that finally results in triggered activation of the systemic acquired resistance response in these plants.

20 (ref. Generation of broad-spectrum disease resistance by overexpression of an essential regulatory gene in systemic acquired resistance. H. Cao et al. 1998. Proc. Natl. Acad. Sci. USA 95: 6531-6536). Recent literature shows the functional interaction between RKS10 and BRI-1, another class 25 of transmembrane LRR receptor kinases (Cell Vol. 110, 213-222 2002). BAK1=RKS10 as described here, interacts with BRI-1 and modulates brassinosteroid signaling; Cell vol 110, 203-212 2002 BRI1/BAK1 a receptor kinase pair mediating brassinosteroid signaling). Brassinosteroids are known to function in a broad range of disease resistance in tobacco and rice (Plant Journal 2003, 887-898). The BRI-1 receptor is involved in the binding of systemin, an 18 amino acid polypeptide, representing the primary signal for the systemic activation of defence genes (PNAS 2002, 9585-9590).

30 35 ELS overexpression phenotypes mimic the effects of inactivation of RKS molecules gene products. Either ELS is competing for ligand binding, or ELS inhibits the interactions

between RKS and BRI-1-like gene products. ELS1 overexpression results in dwarf phenotypes in Arabidopsis and tobacco plants, similar as observed for antisense RKS4 and RKS10, and for knock out plants of RKS0 and RKS4.

- 5 Deregulating expression of ELS and / or RKS genes in plant would modify the broad spectrum disease resistance in such plants. This would explain the observed data that brassinosteroids are involved in disease resistance (Plant Journal 2003, 33 887-898.)

Further references

- Plant Journal 1997: 12, 2 367-377
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5 Gene 1999, 237, 91-104
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Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

Claims

1. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying

5 expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein or encoding a protein comprising a ligand for said complex.

10

2. A method according to claim 1 allowing modulating cellular division during plant growth or organ formation

15 3. A method according to claim 2 wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent thereof.

4. A method according to claim 1 allowing modulating apical meristem formation.

20 5. A method according to claim 4 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof.

25 6. A method according to claim 4 allowing modulating fasciation.

7. A method according to claim 6 wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof.

30

8. A method according to claim 4 allowing modulating root development.

35 9. A method according to claim 7 wherein said gene comprises an ELS1, ELS 2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof.

10. A method according to claim 4 allowing modulating
meristem identity.

11. A method according to claim 9 wherein said gene comprises
5 an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent
thereof.

12. A method according to claim 1 allowing modulating pollen
development.

10

13. A method according to claim 11 wherein said gene
comprises an ELS2 or RKS10 gene or functional equivalent
thereof.

15

14. A method for providing resistance to a plant or plant
cell comprising modifying a gene or modifying expression of
said gene, wherein said gene is encoding a protein belonging
to a signalling complex comprising NDR/NHL protein, or encoding
a protein comprising a ligand for said complex.

20

15. A method for obtaining a plant or plant cell with a
modulated development comprising subjecting a plant or plant
cell to a method according to anyone of claims 1 to 13.

25

16. A method for obtainig a resistant plant or plant cell
comprising subjecting a plant or plant cell to a method
according to claim 14.

30

17. A plant or plant cell obtainable with a method according
to claim 15 or 16.

Fig. 1

Different domains of RKS proteins

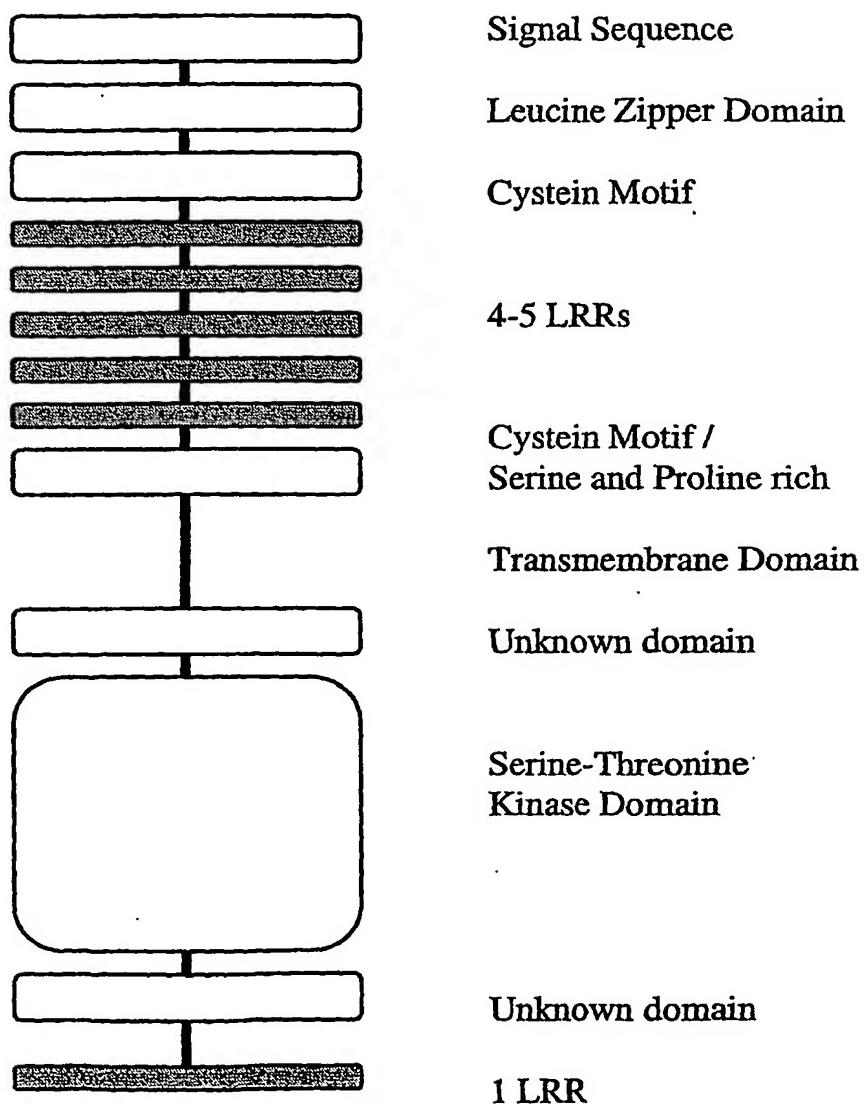


Fig. 2

Developmental tree of the different Receptor Kinases like SERK (RKS) genes.

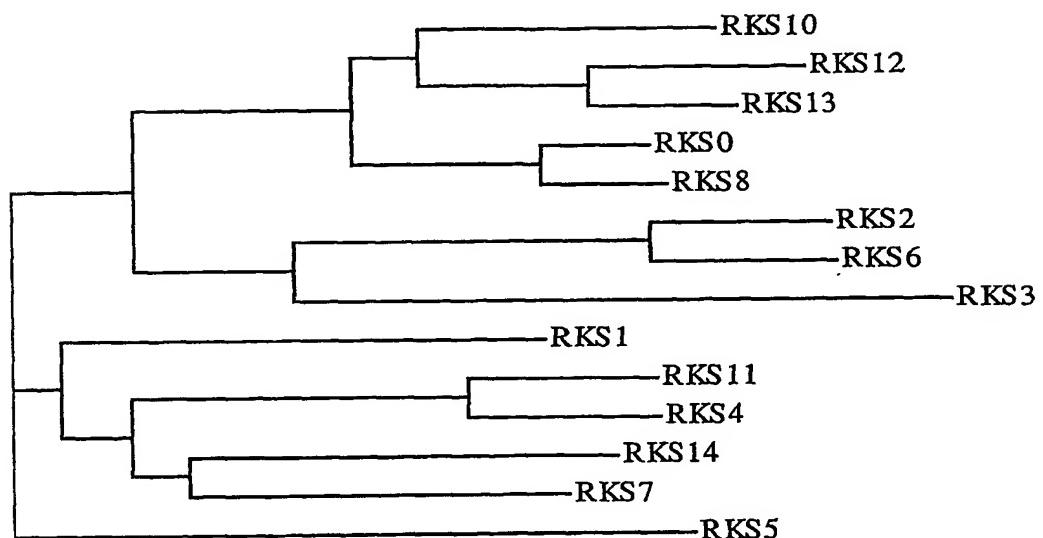
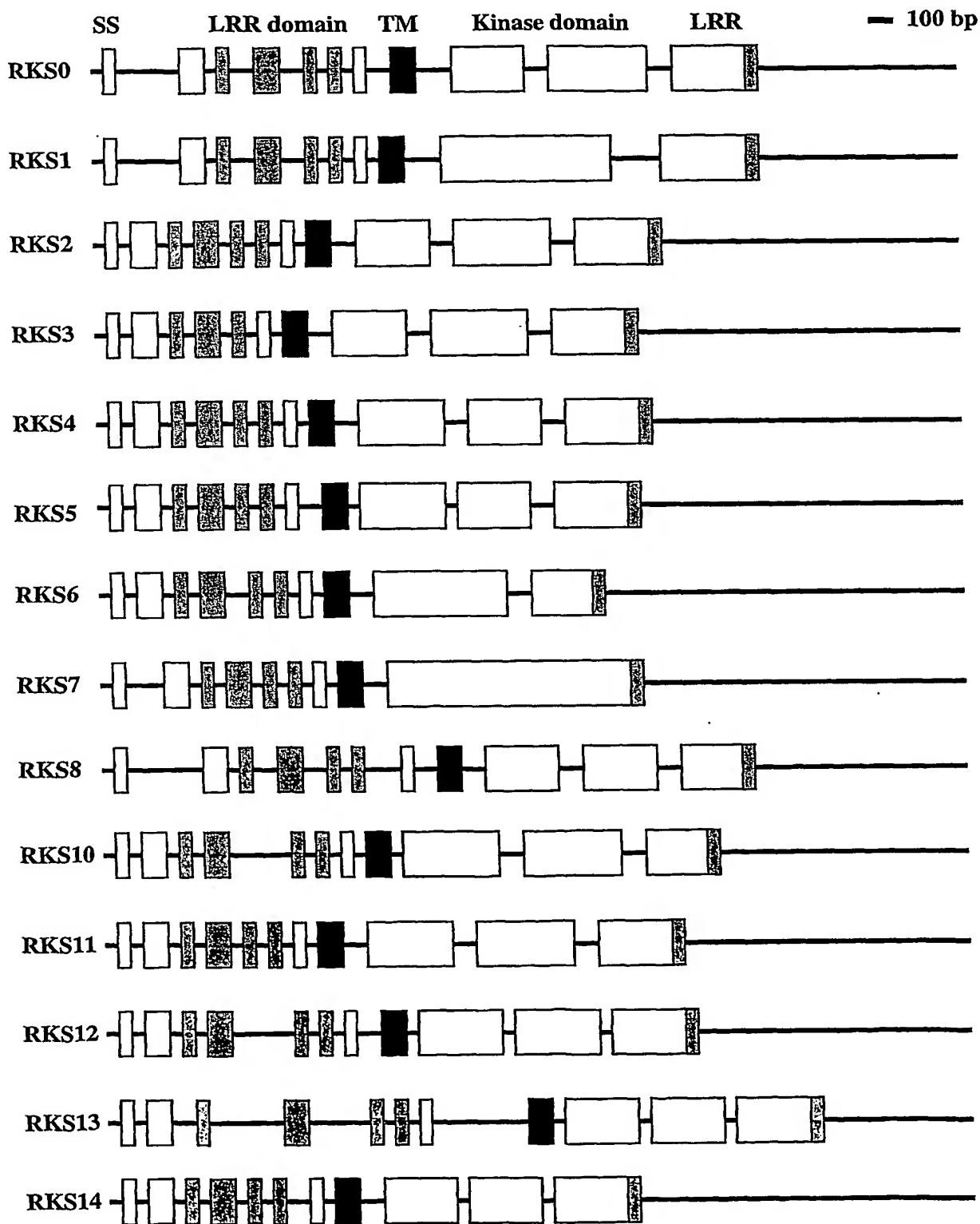
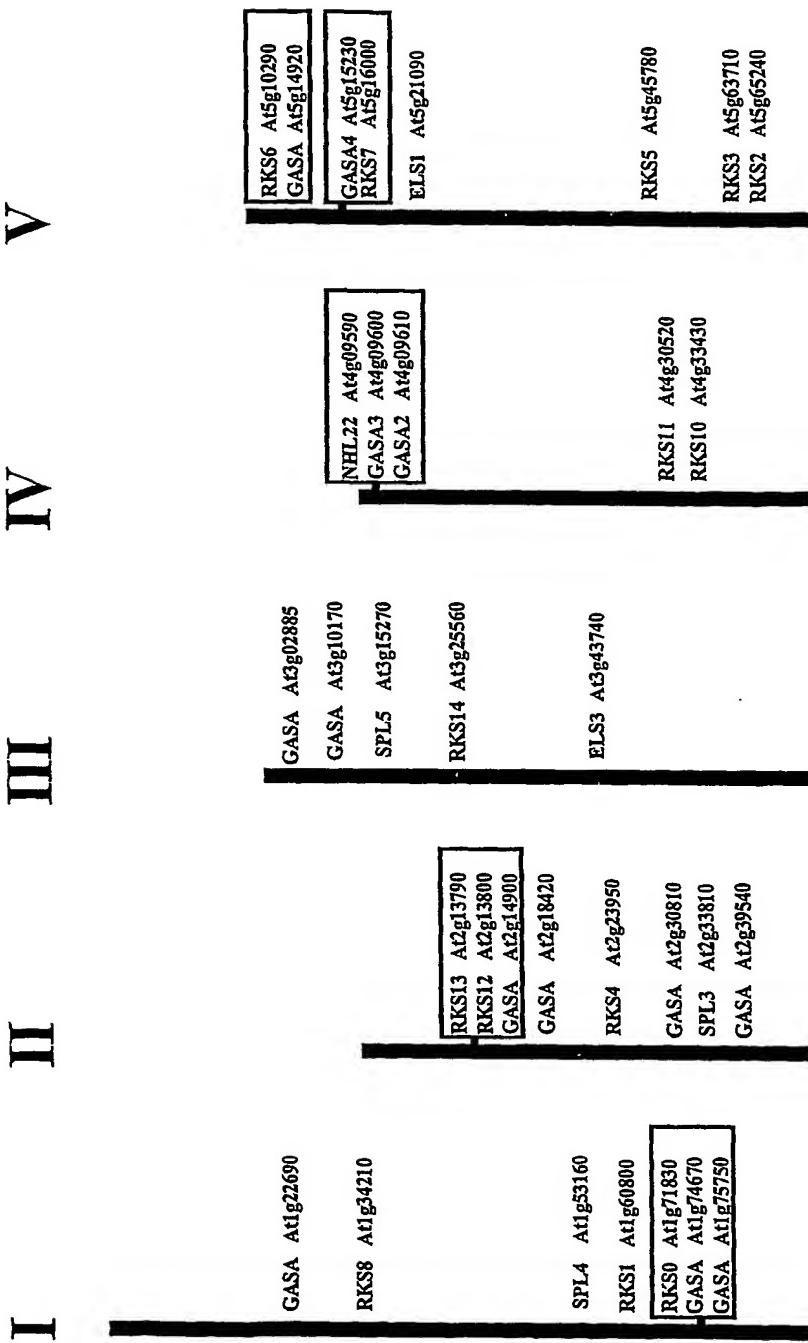


Fig. 3

Intron-Exon structure of the RKS genes in *Arabidopsis thaliana* var. Columbia.
SS signal sequence; LRR leucine rich repeat domain; TM transmembrane domain.

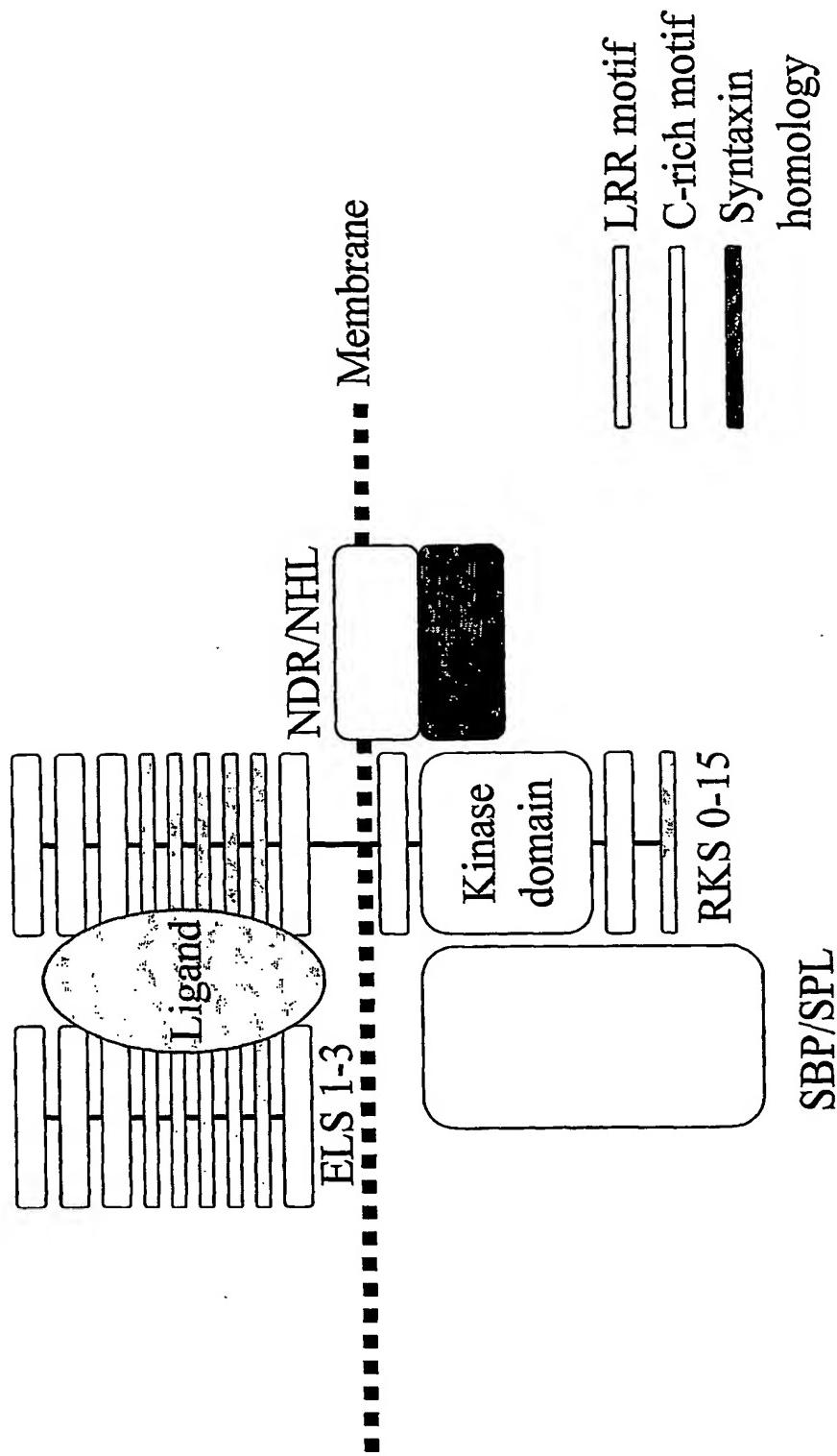


**Chromosomal location of RKS genes
in *Arabidopsis thaliana***

**Fig. 4**

RK5-mediated signal transduction
pathway in plants

Fig. 5



GT-RKS4 determines seedling size
in *Nicotiana tabacum*.

Modifications in the
expression profile
of GT-RKS4 modulates
organ size within seedlings
of *Nicotiana tabacum*.

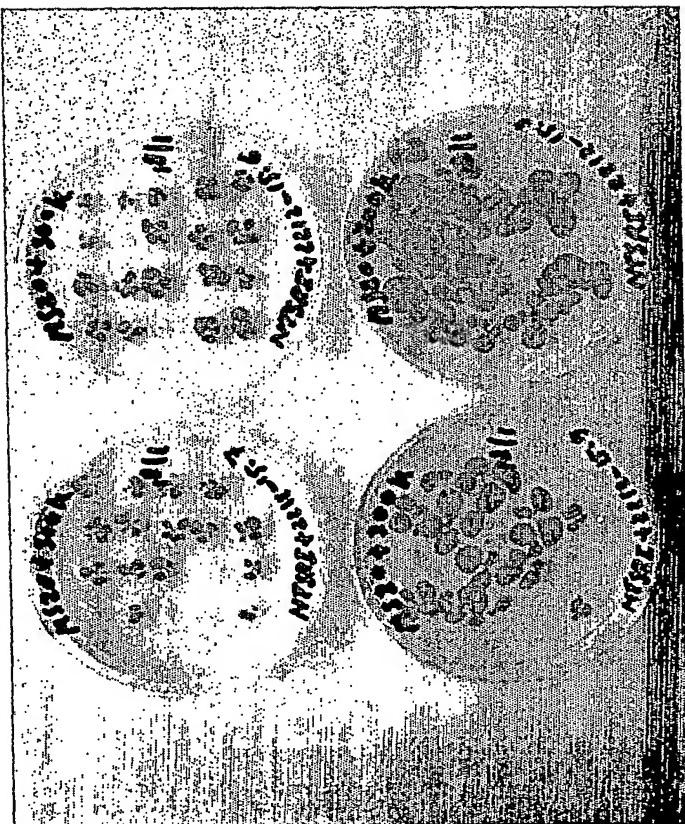


Fig. 7

GT-RKS4 determines organ size
in *Nicotiana tabacum*.

GT-RKS4-7S-T2

GT-RKS4-6S-T2

GT-RKS4-3S-T2

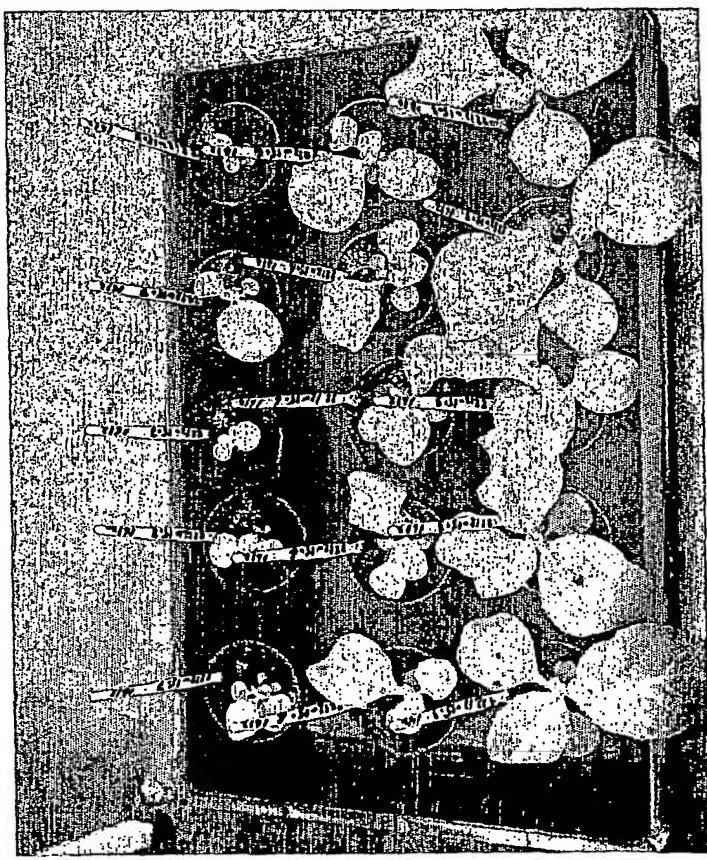
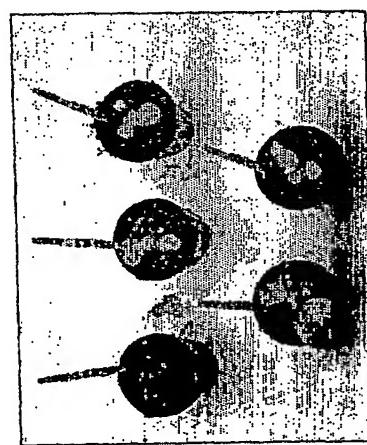
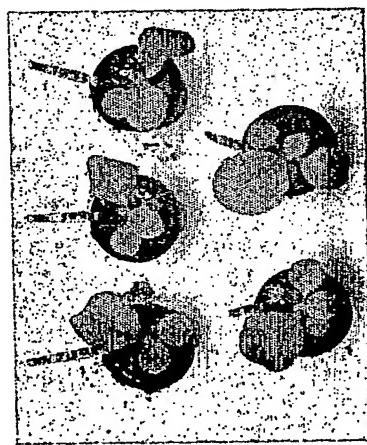
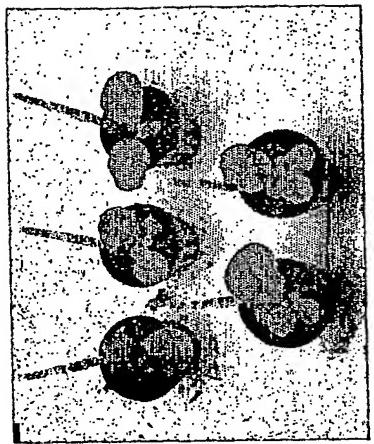


Fig. 8

GT-RKS4 determines plant size
in *Nicotiana tabacum*

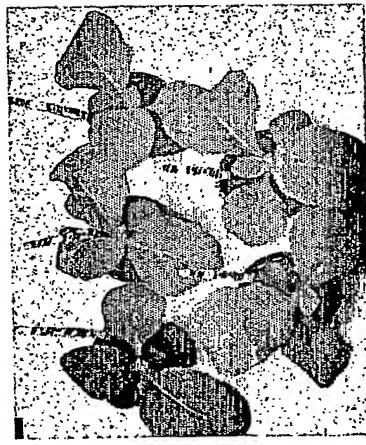


GT-RKS4-15S-6T2

GT-RKS4-15S-7T2

GT-RKS4-15S-9T2

Empty vector control

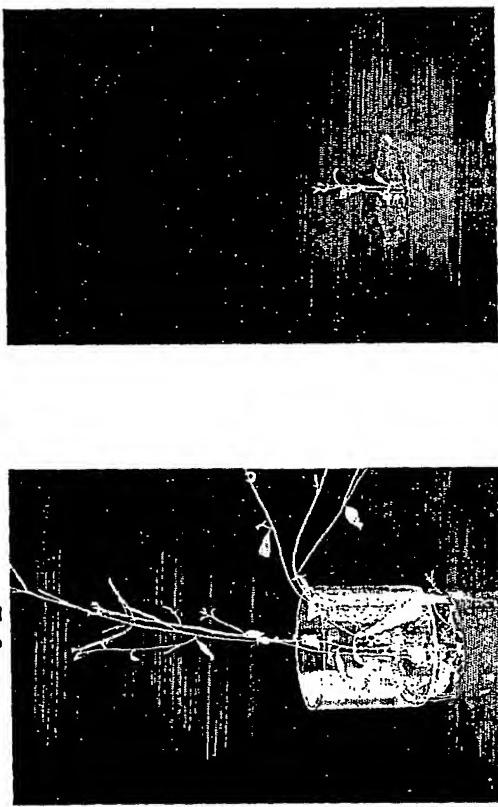


GT-RKS4-15S-3T2

Fig. 9

Stable transformed GT-RKS4-antisense
in *Arabidopsis thaliana*

Wildtype WS



Overexpression of antisense GT-RKS4-1a
reduces plant and organ size.

Fig. 10

Ectopic expression of RKS4 and GASA3 gene products both result in increases flower size in *Arabidopsis thaliana* WS

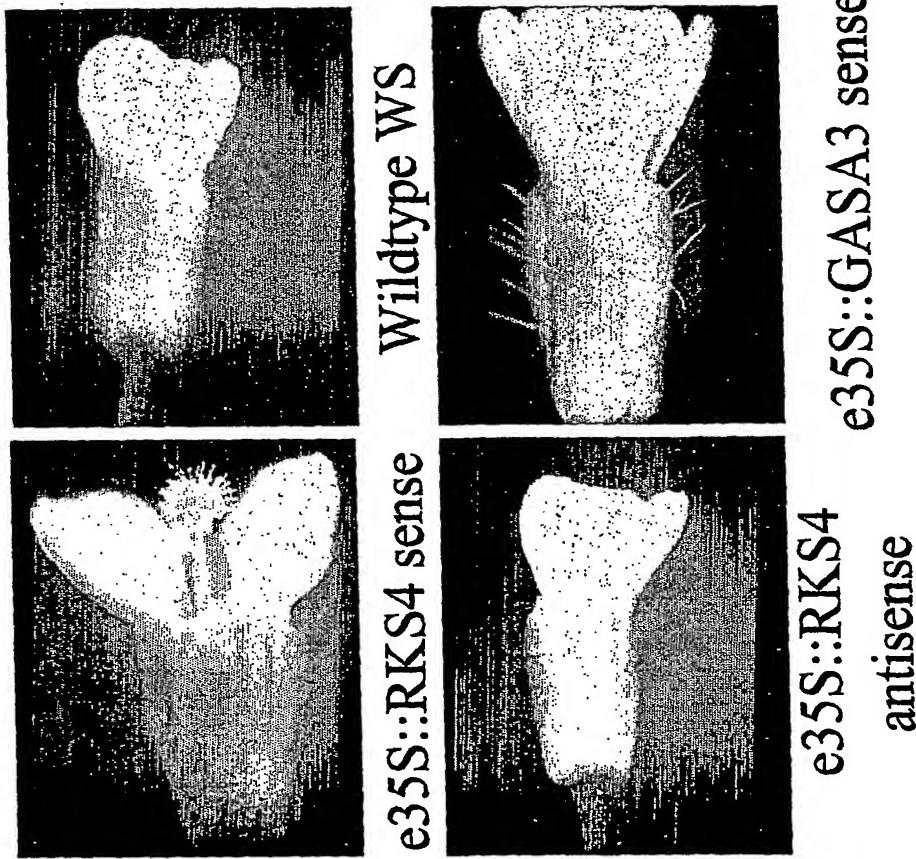


Fig. 11

Ectopic expression of RKS4 in seedlings results in the formation of meristematic regions in the hypocotyl of *Arabidopsis thaliana* WS

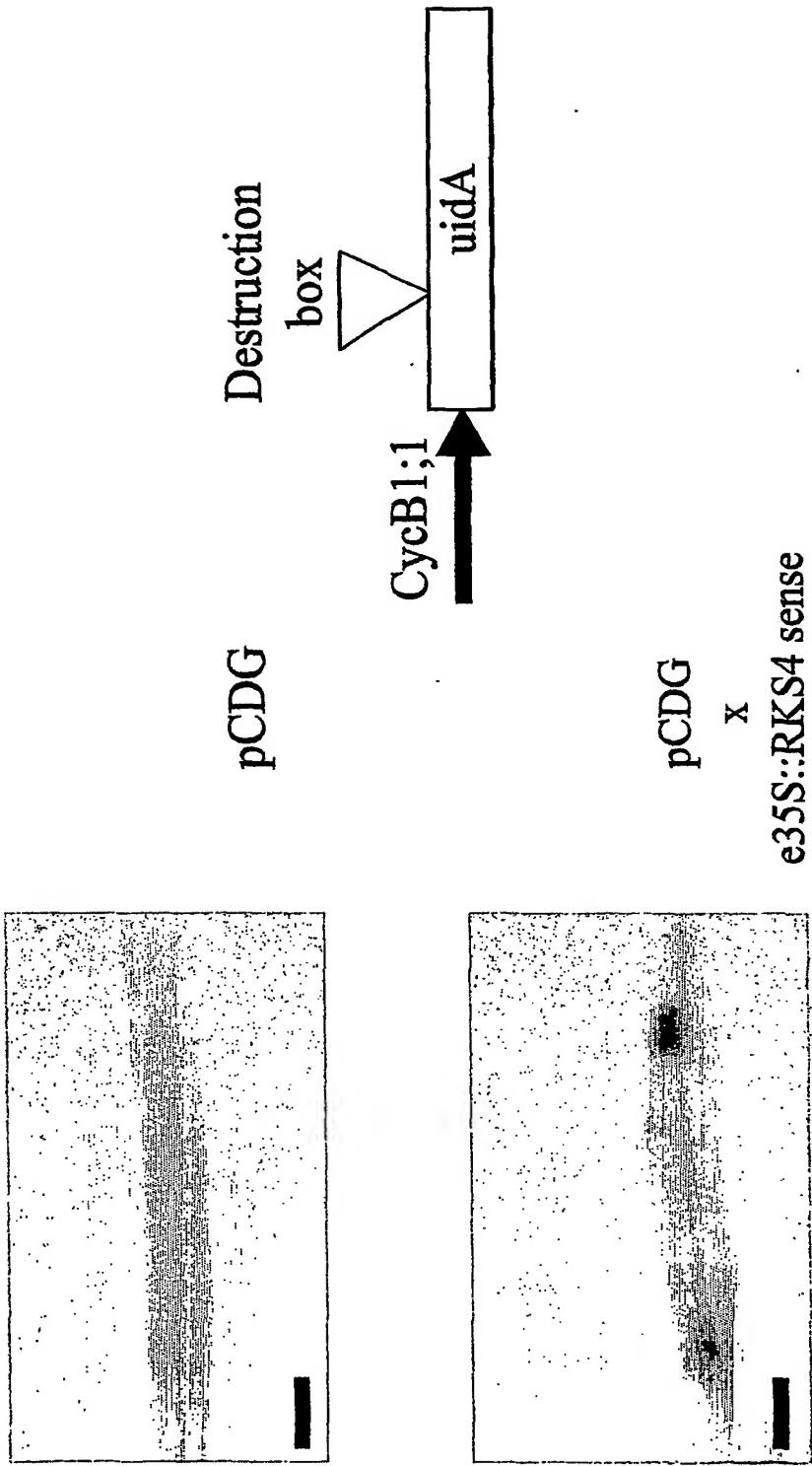


Fig. 12

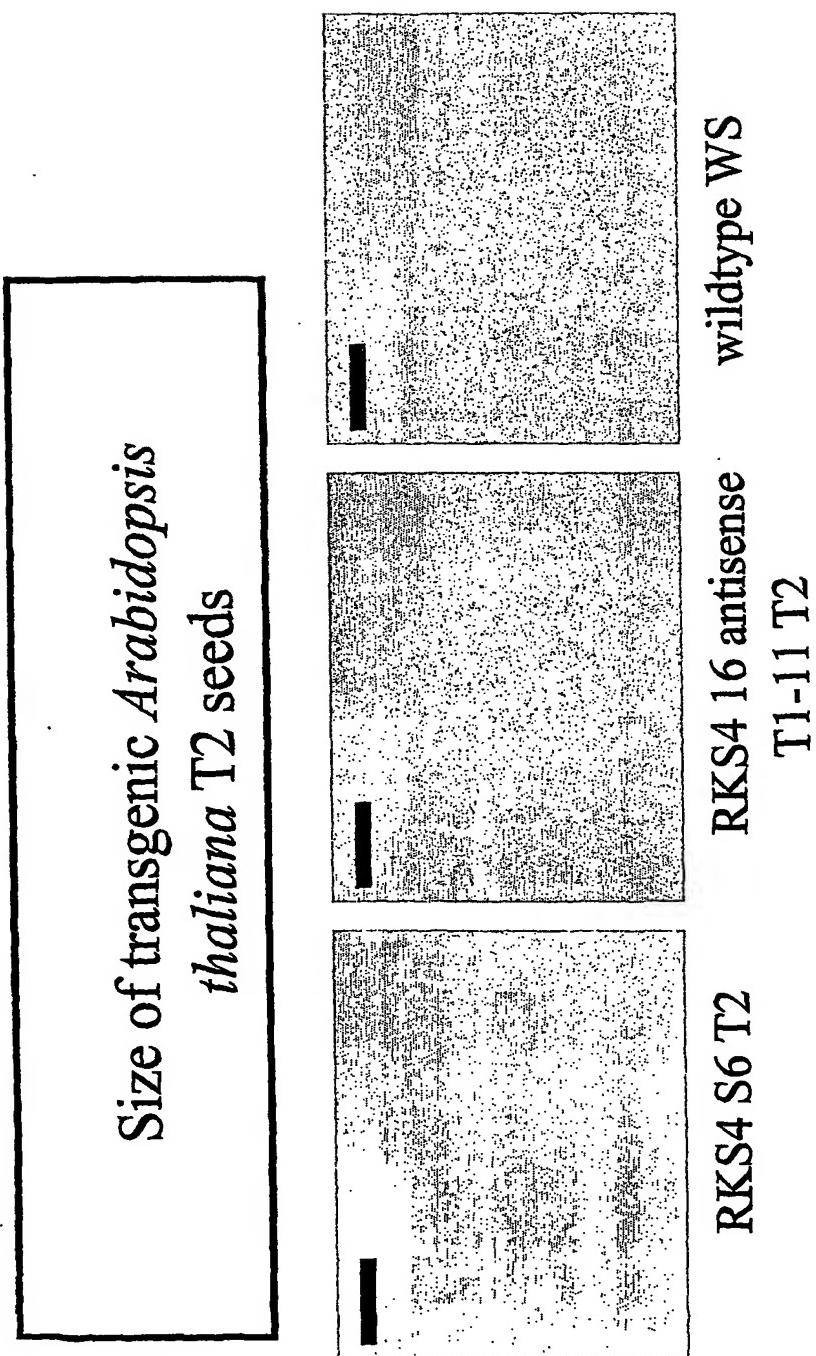


Fig. 13

RKS4 regulates cell number and cell size in *Arabidopsis thaliana*.

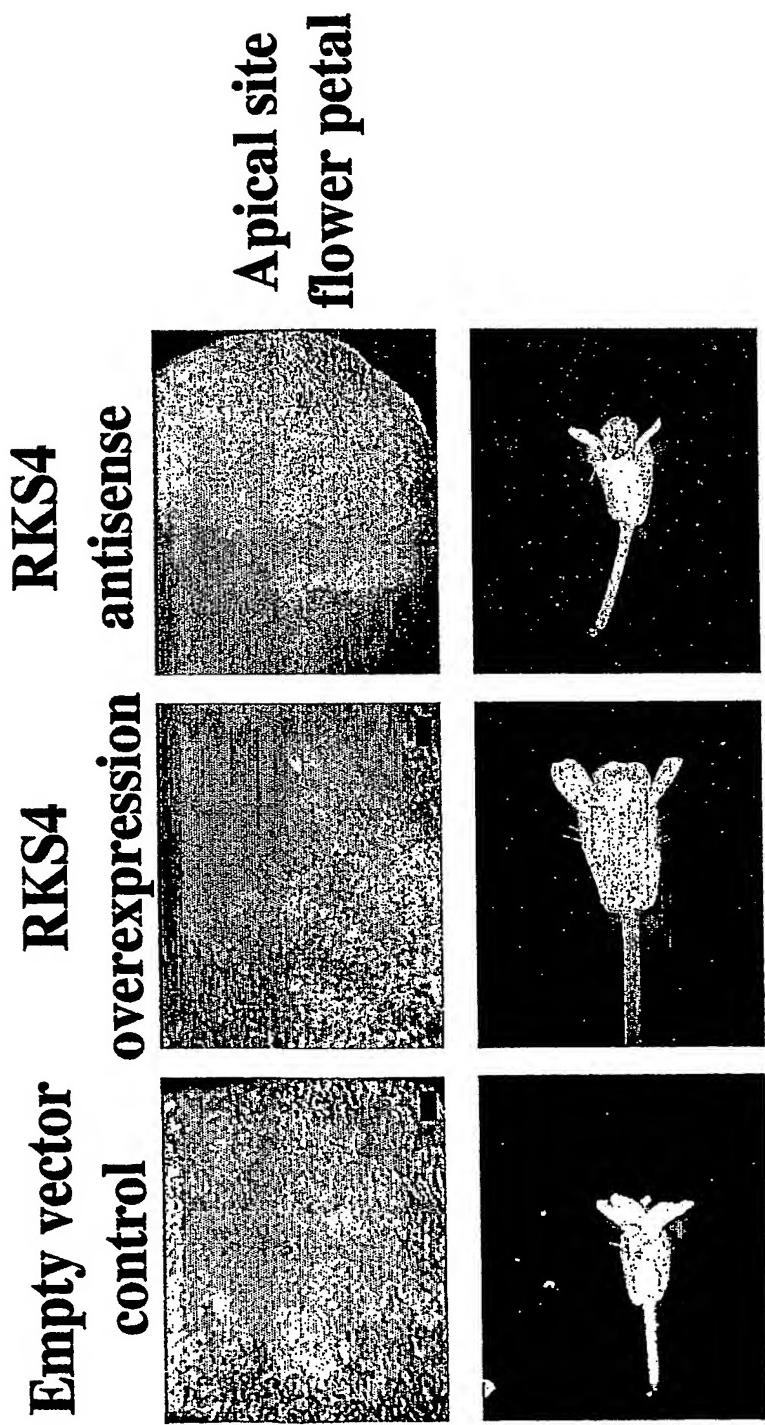
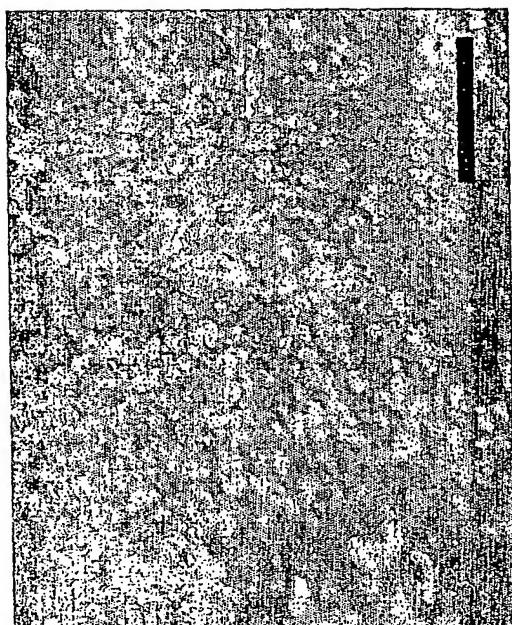
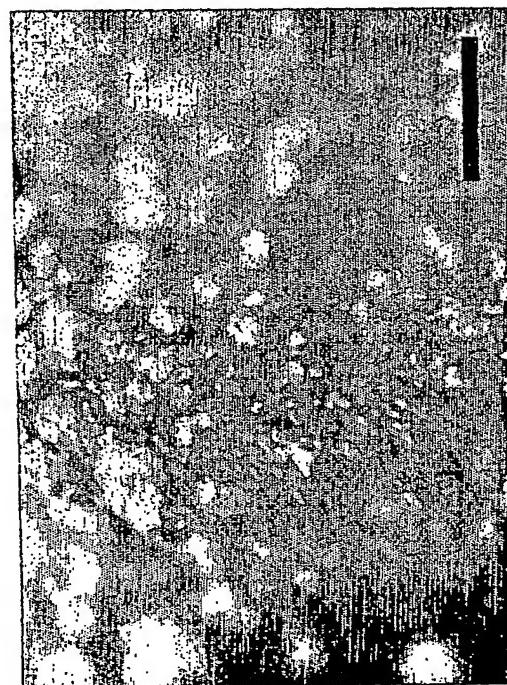


Fig. 14

RKS10S T1-10
results in a decrease in size
of cotyl-like apical epidermal cells



RKS10S T1-10



pGreen 4K

Fig. 15

RKS10 antisense T1-4
results in an increase in size
of the cotyl epidermal cells

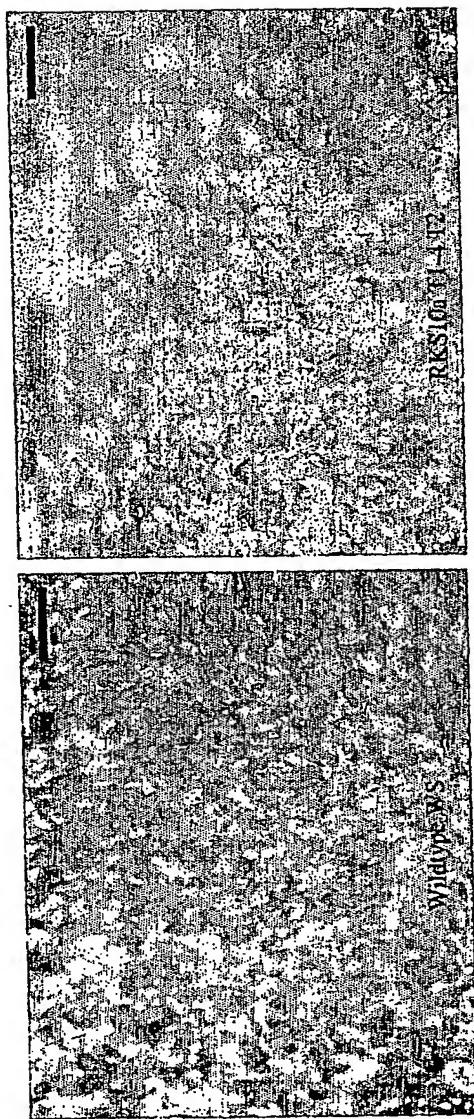


Fig. 16

Flower development from the same
influorescence in transgenic
Arabidopsis thaliana

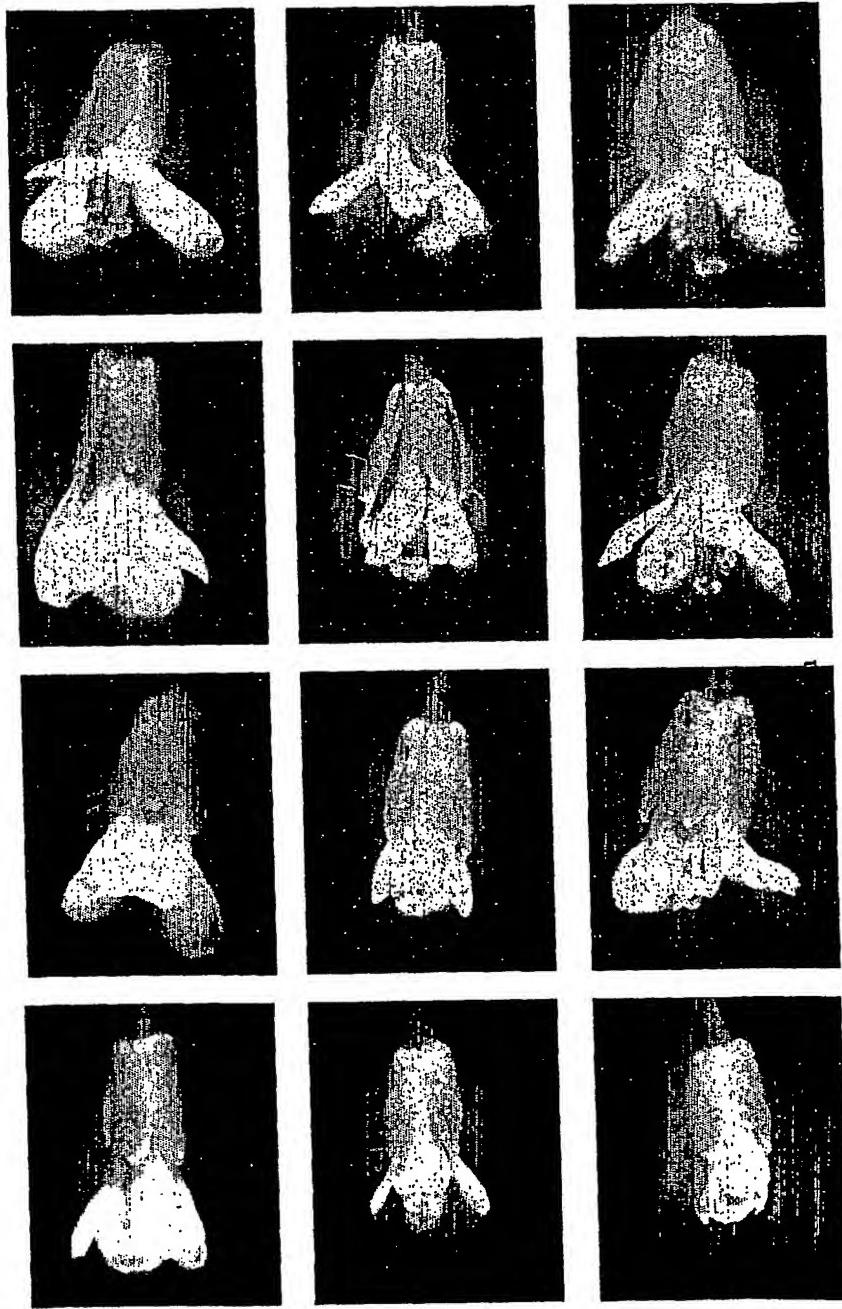


Fig. 17

Regeneration potential of
Arabidopsis transgenic seedlings.

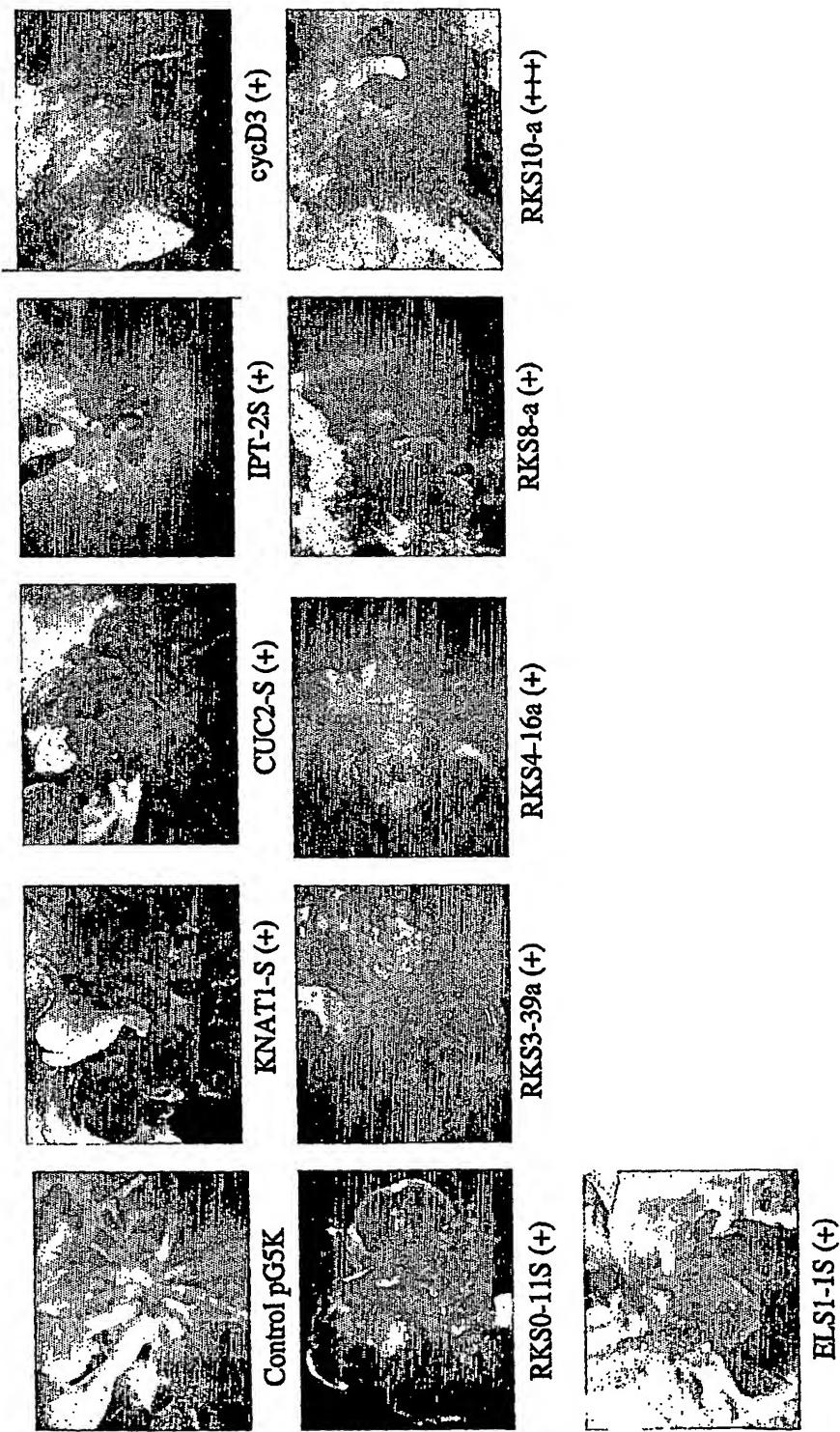


Fig. 18

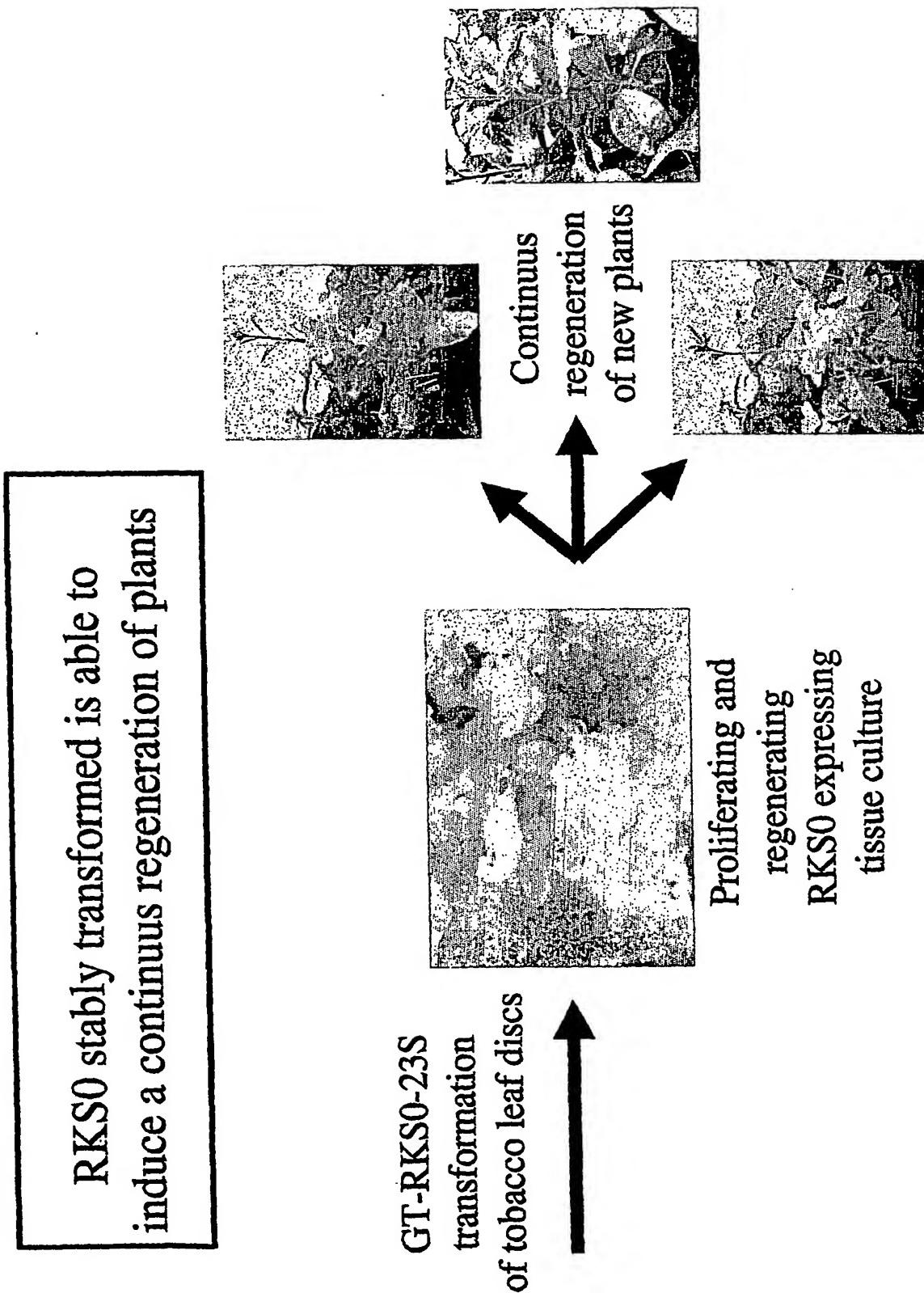


Fig. 19

Fasciation in transgenic
Arabidopsis thaliana

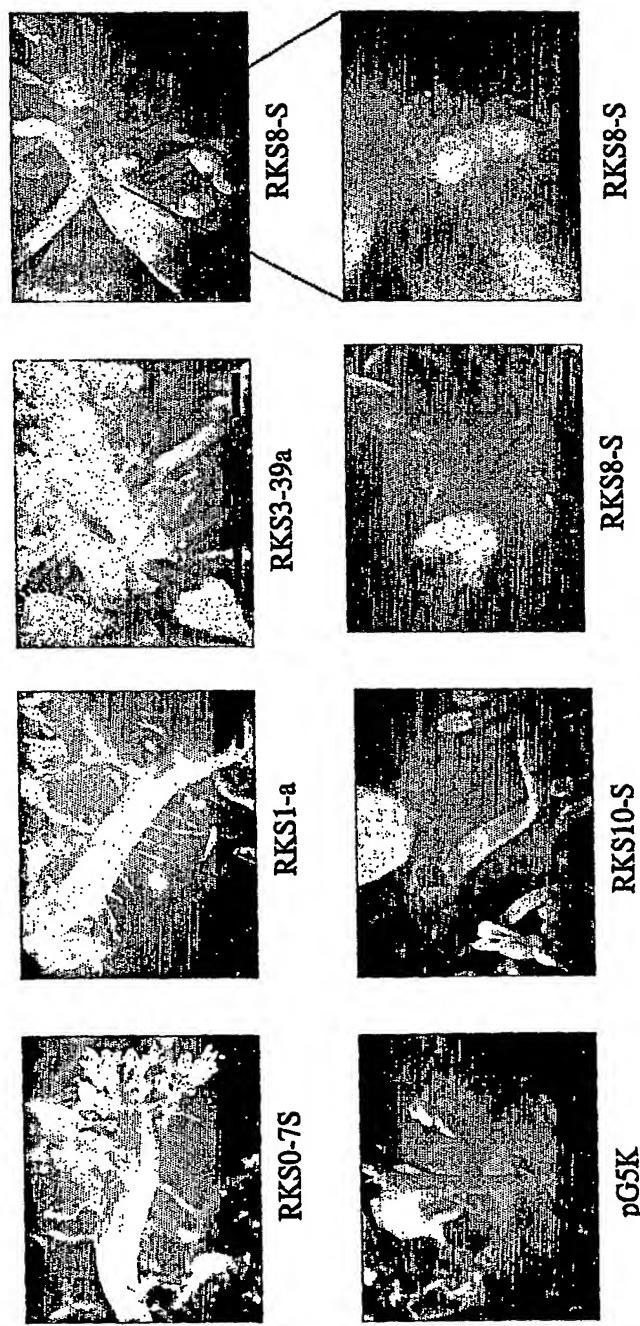


Fig. 20

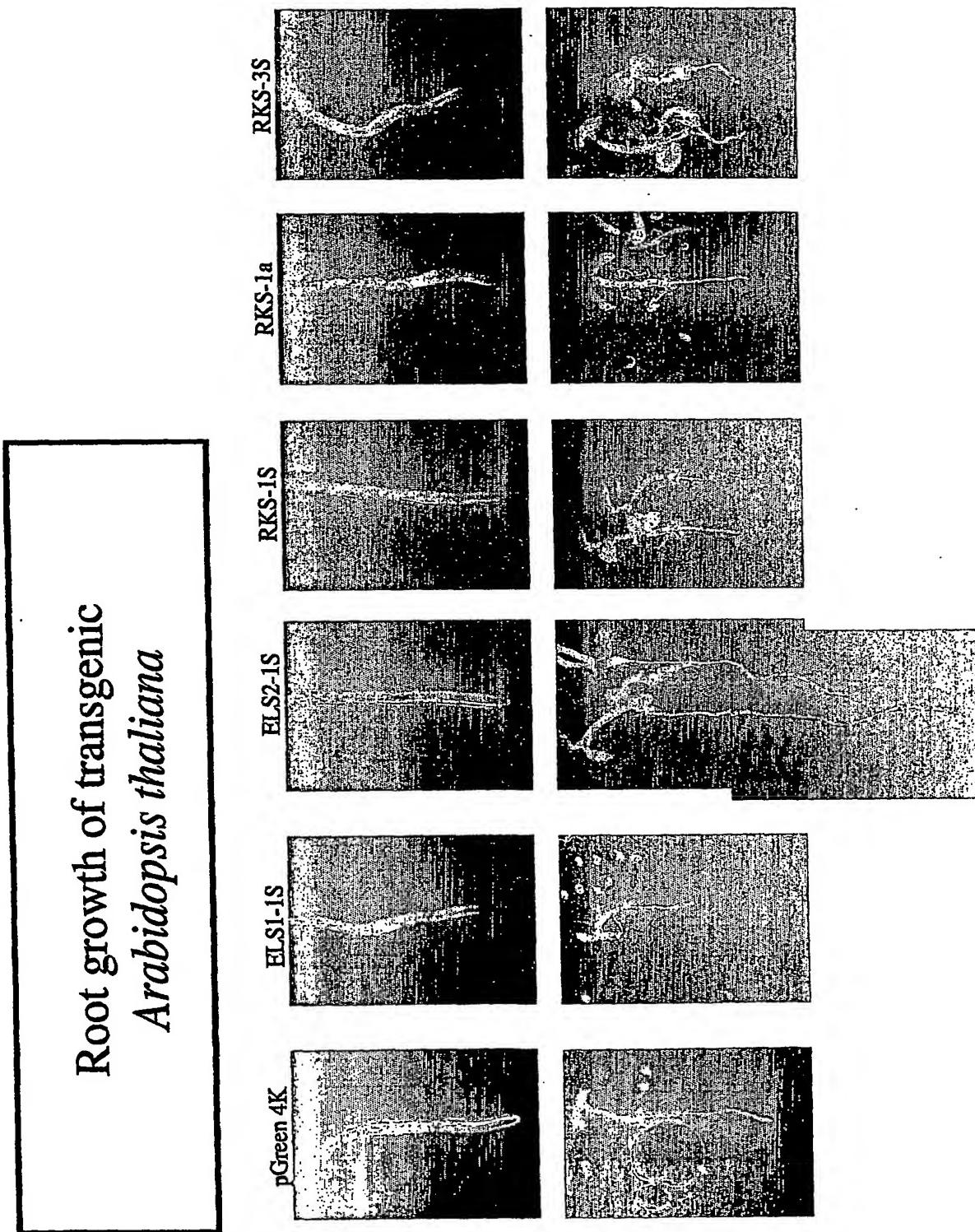


Fig. 21

Root growth of transgenic
Arabidopsis thaliana

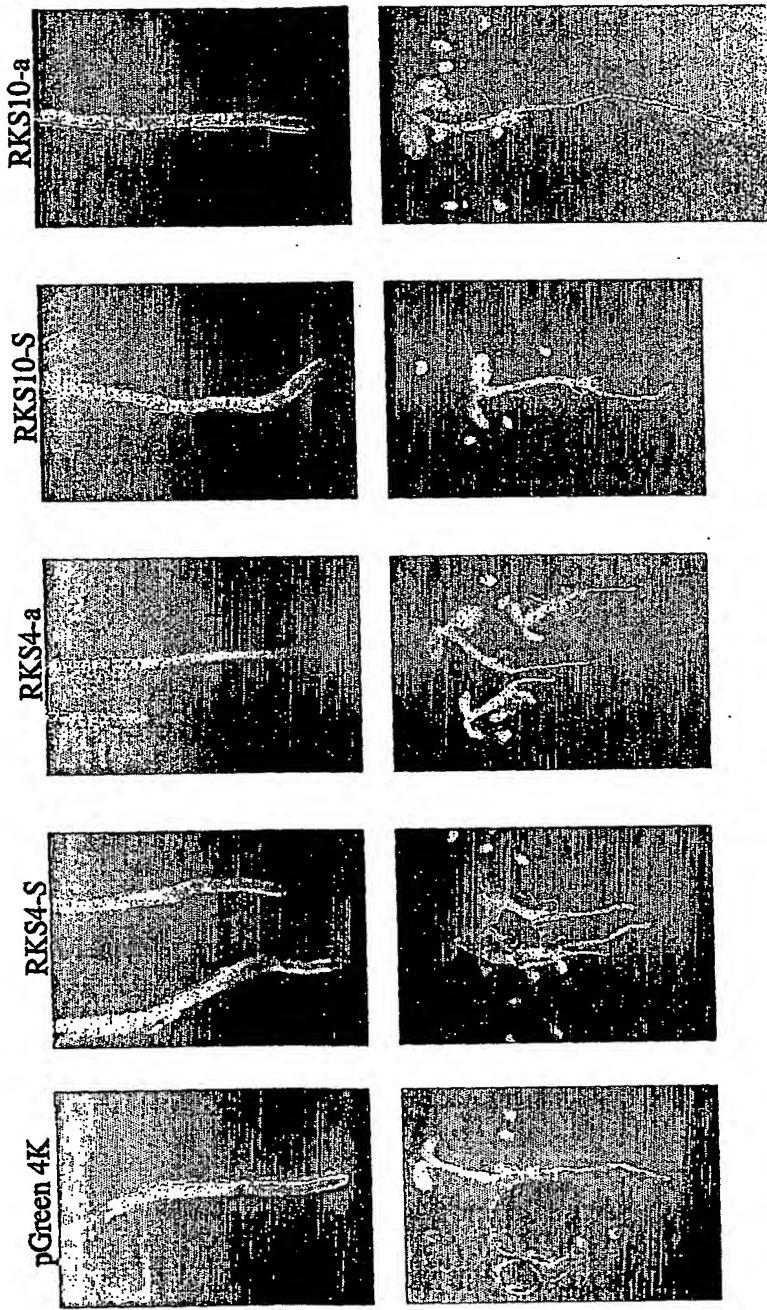


Fig. 22

Root growth of transgenic
Arabidopsis thaliana

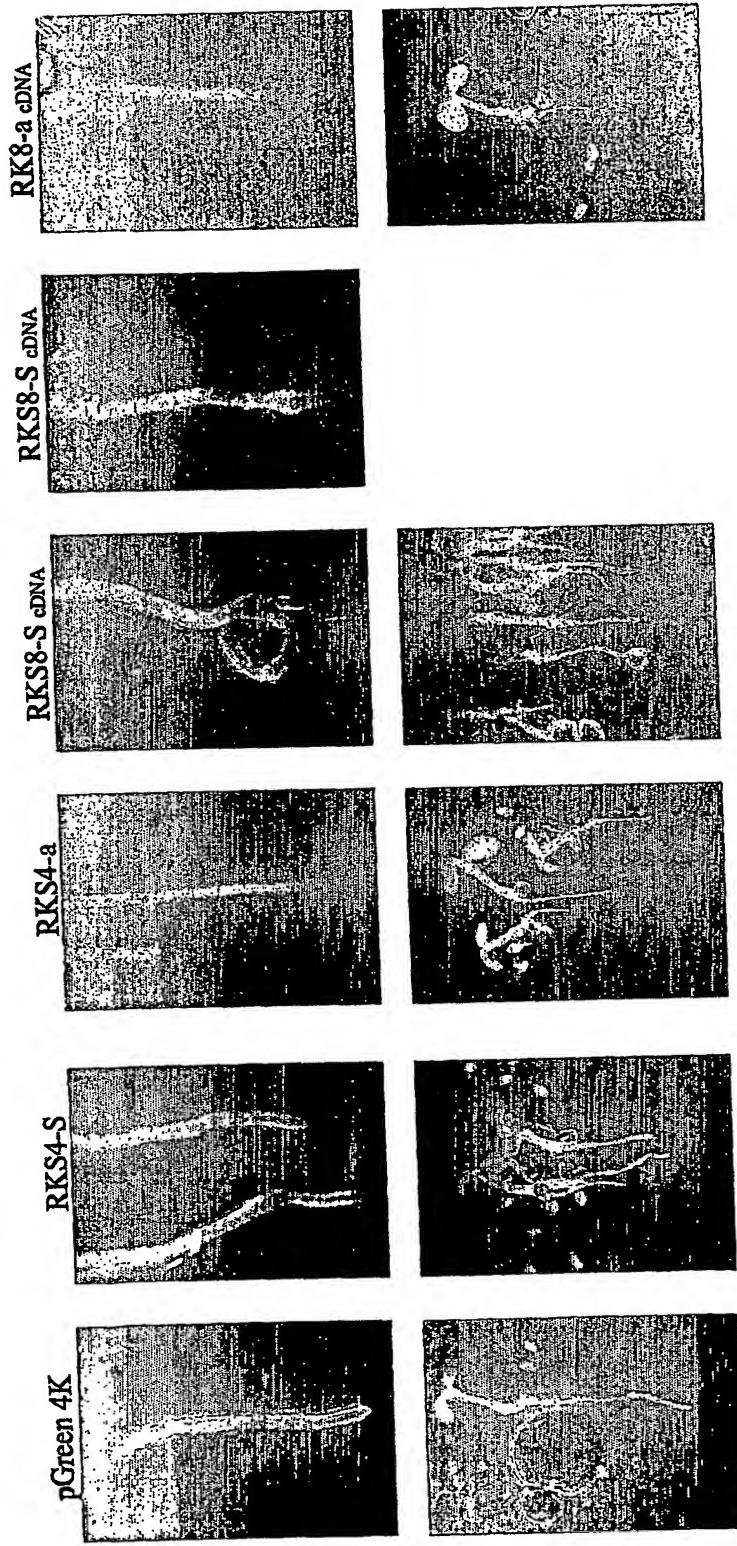


Fig. 23

Root growth of transgenic
Arabidopsis thaliana

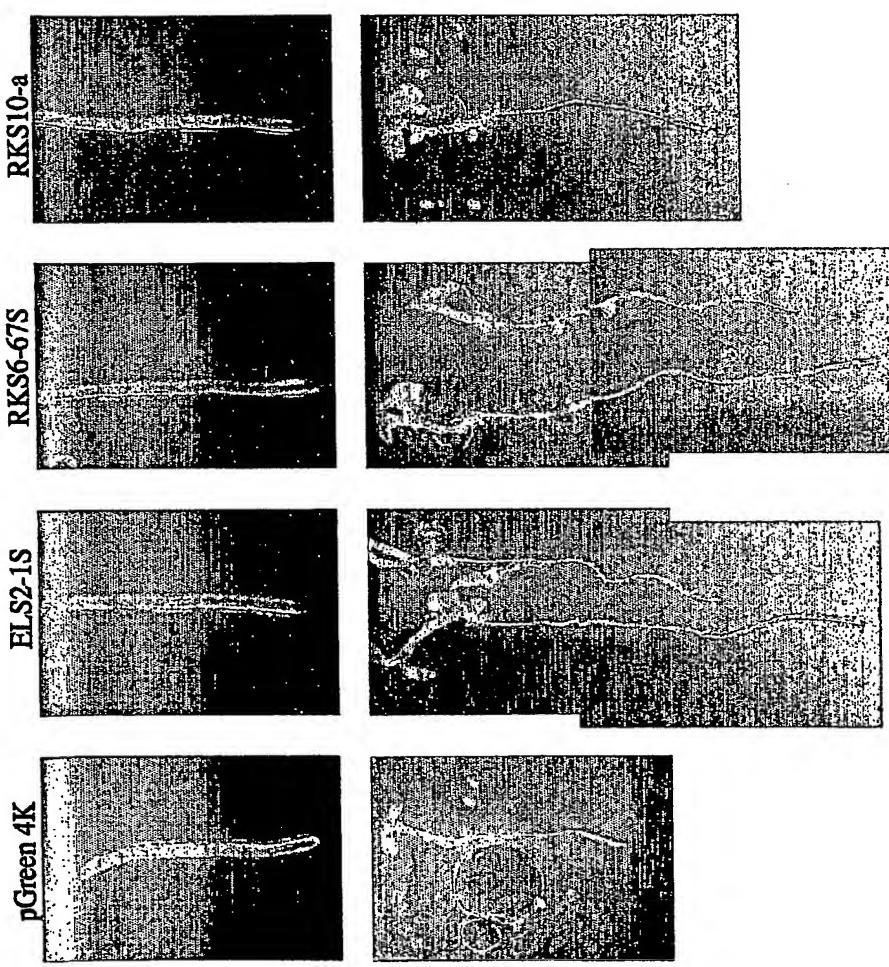
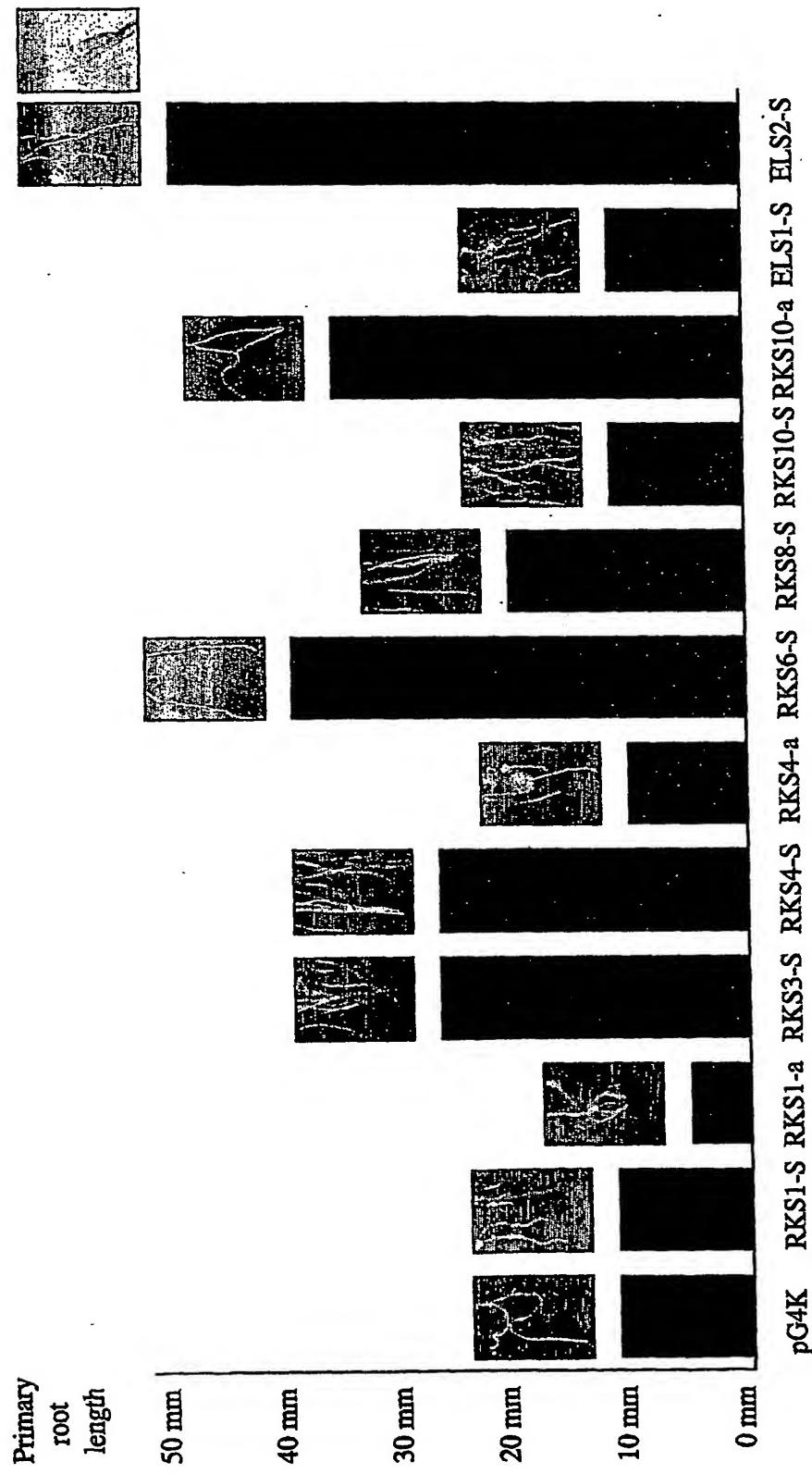
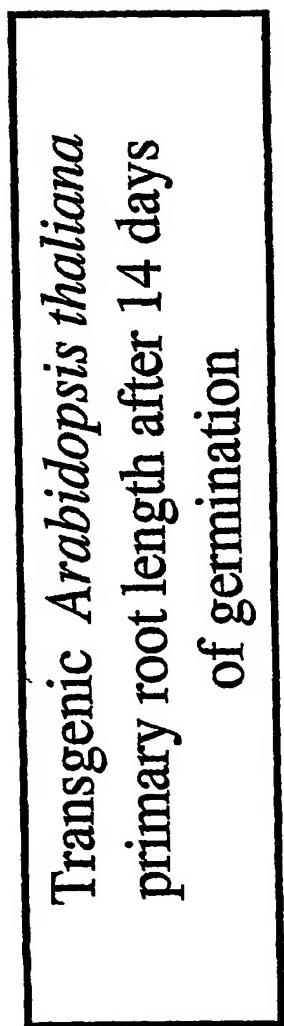


Fig. 24



Transgenic construct

Fig. 25

Effects of RKS10 transgenic constructs on plant development of 45 days old *Arabidopsis* WS

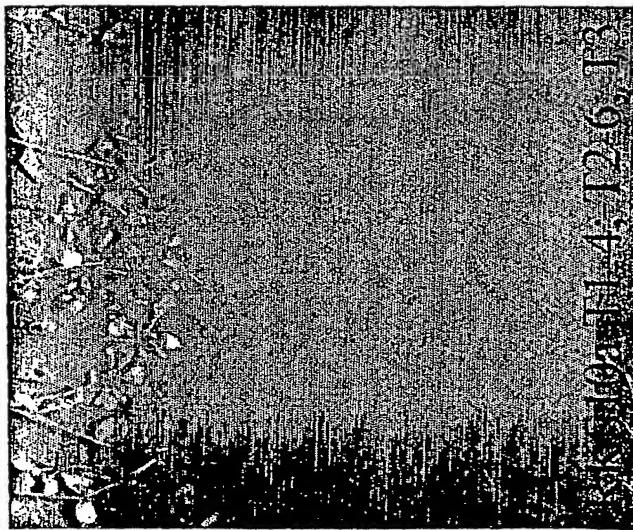
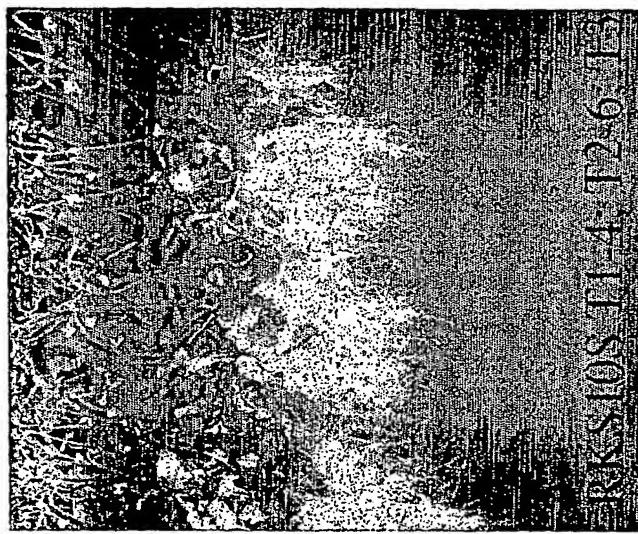


Fig. 26

Roots of Transgenic
Arabidopsis thaliana

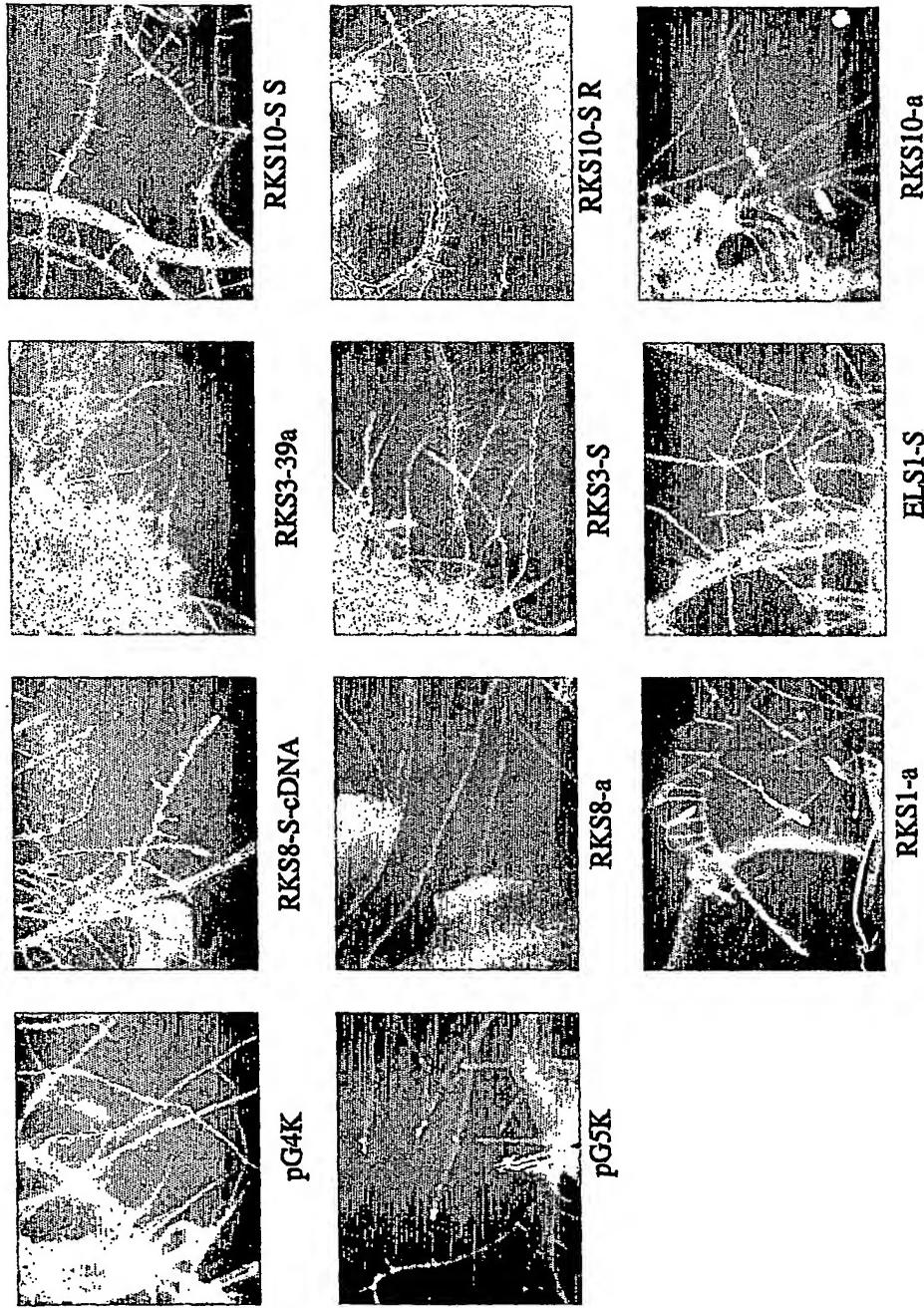


Fig. 27

Root cells of transgenic
Arabidopsis thaliana

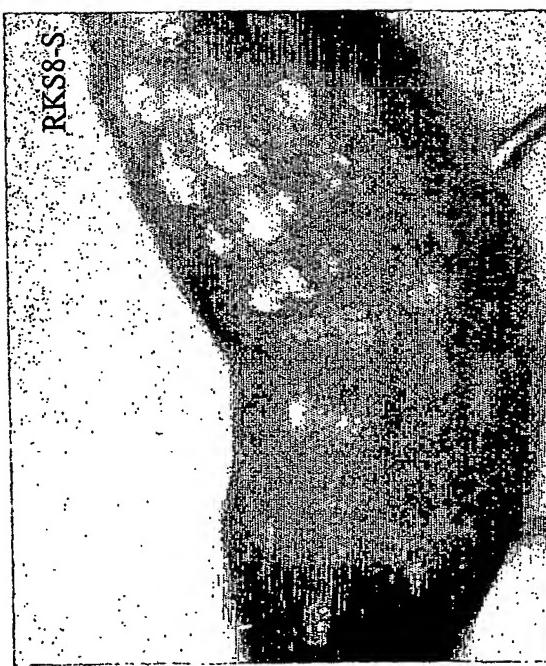
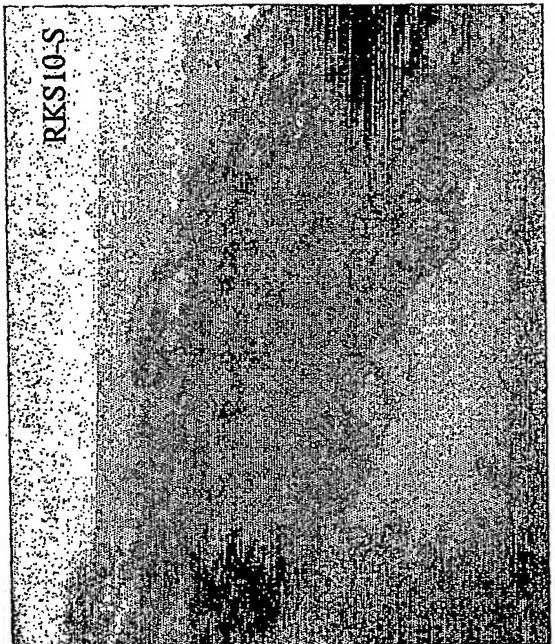


Fig. 28

Influorescences of T1 transgenic
Arabidopsis WS plants

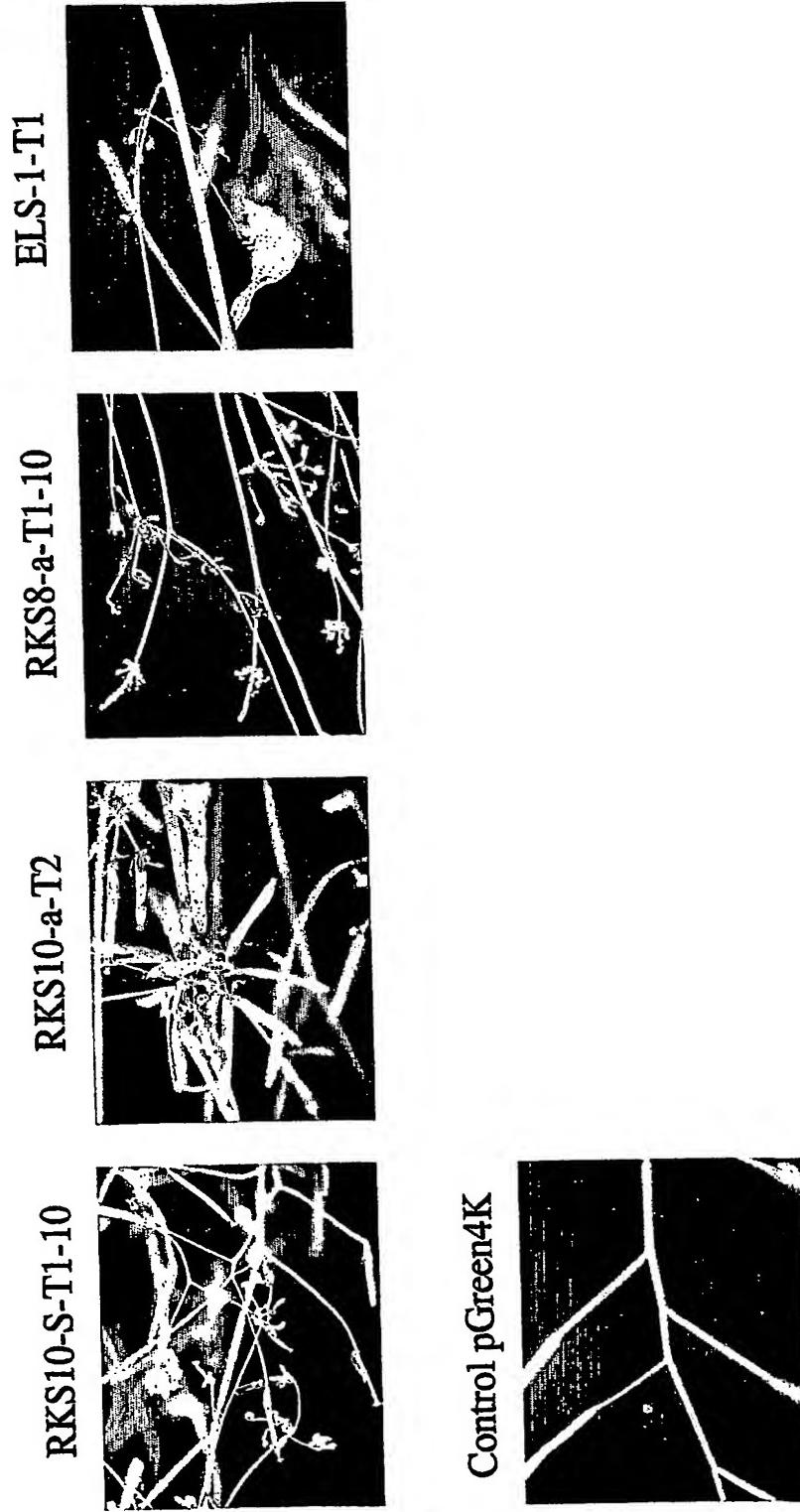


Fig. 29

Influorescences of T1 transgenic
Arabidopsis WS plants

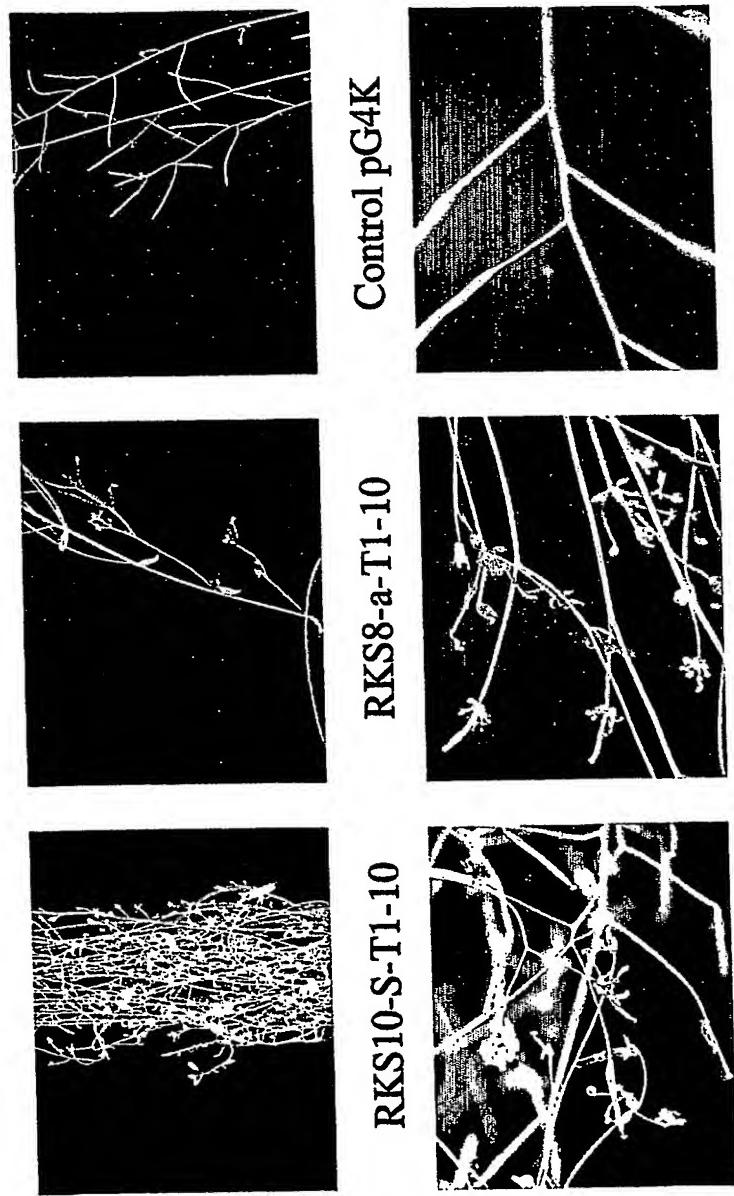


Fig. 30

RKS10a T1 expression constructs in
Arabidopsis thaliana

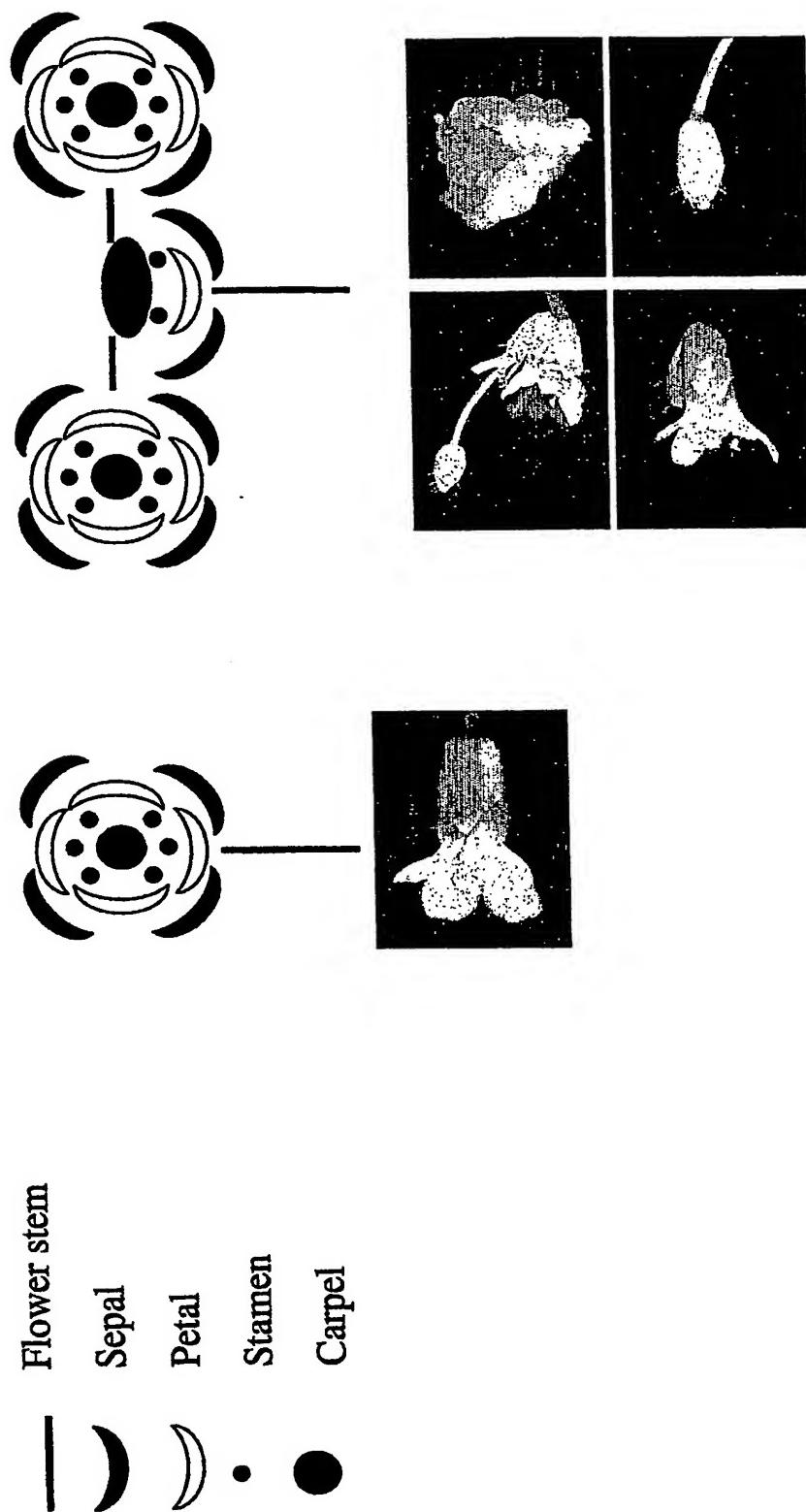


Fig. 31

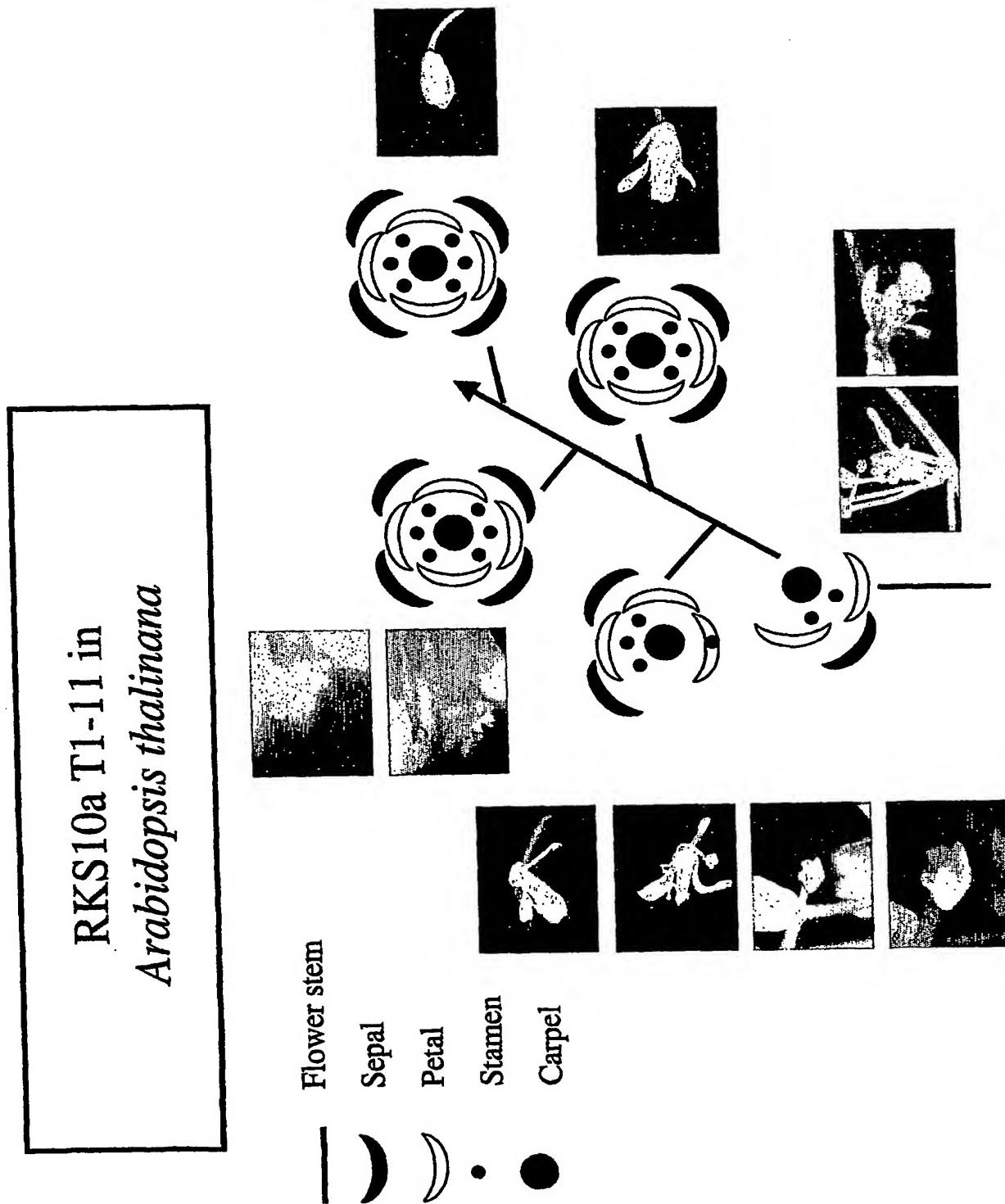
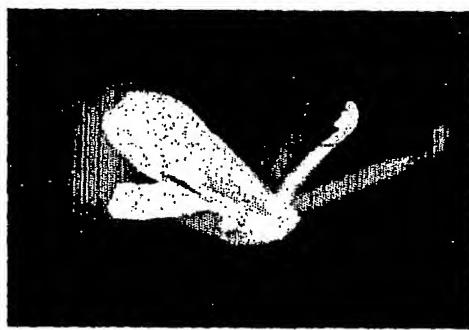


Fig. 32

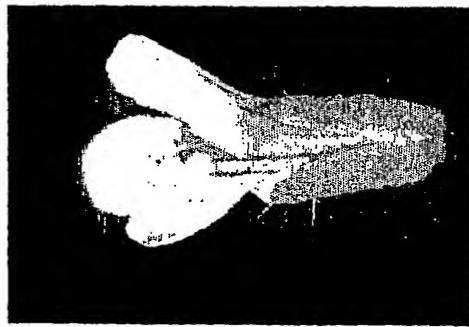
RKS10 antisense effects in
Arabidopsis thaliana



detail flower RKS10a T1-11



RKS10a T1-11



pGreen 4K

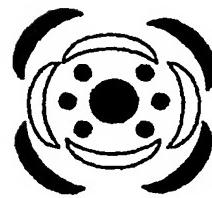


Fig. 33

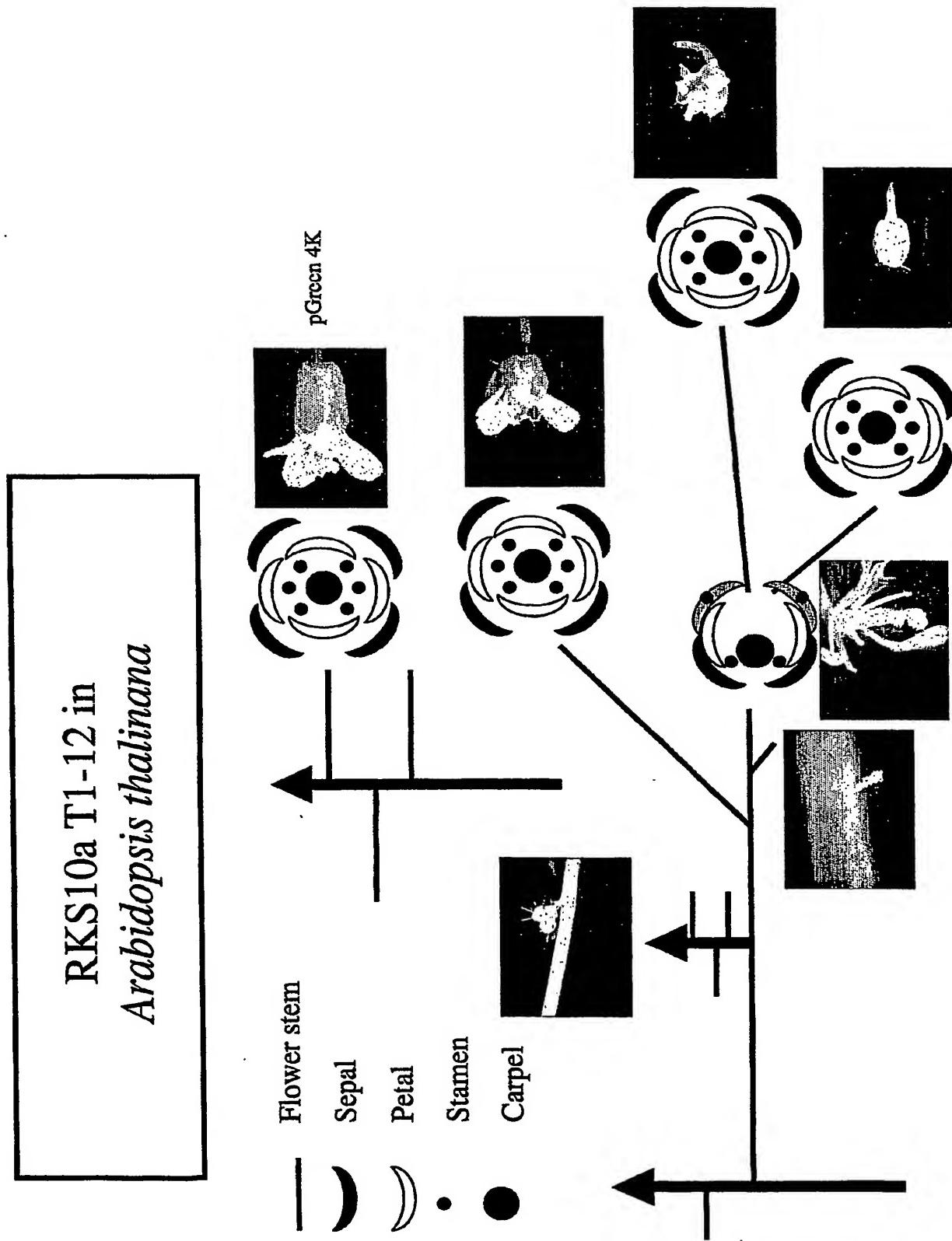


Fig. 34

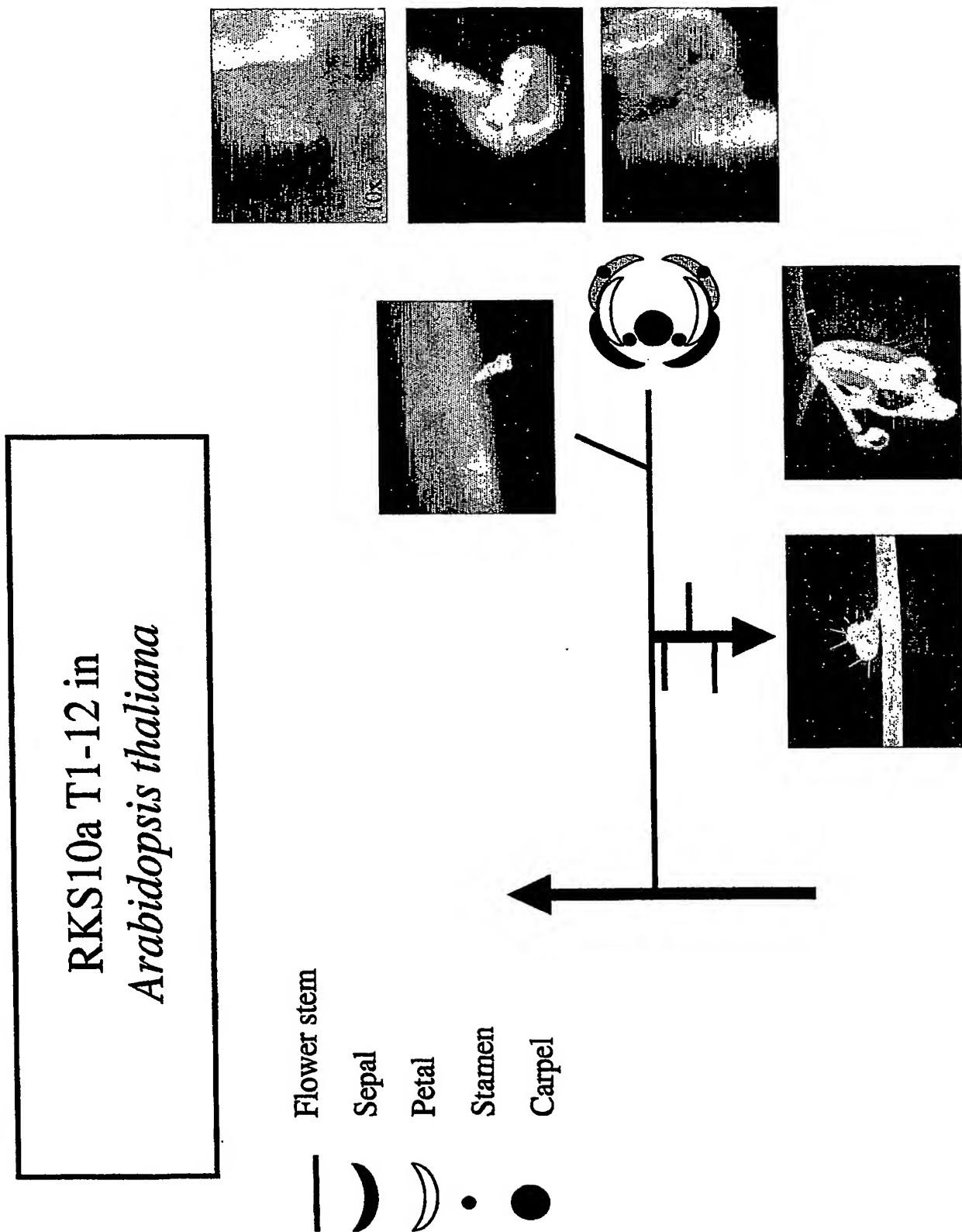


Fig. 35

RKS13 regulates
flower meristem identity in
Arabidopsis thaliana

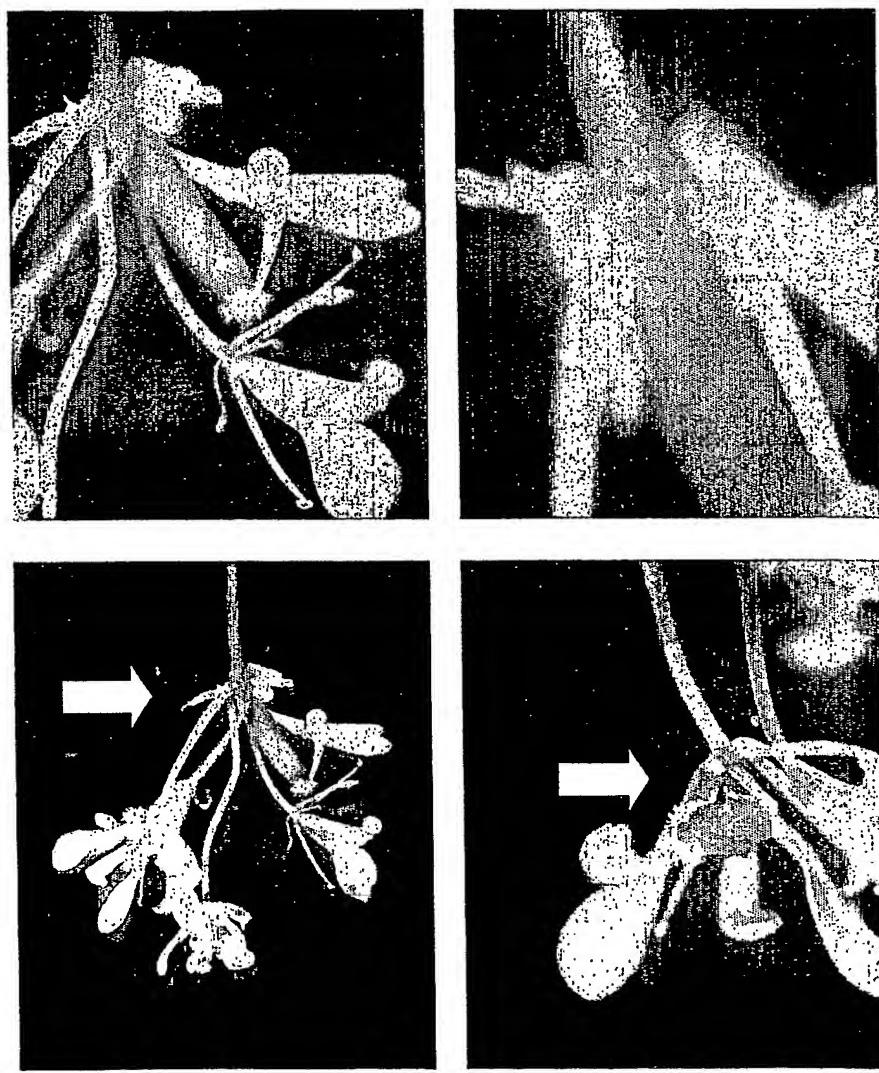
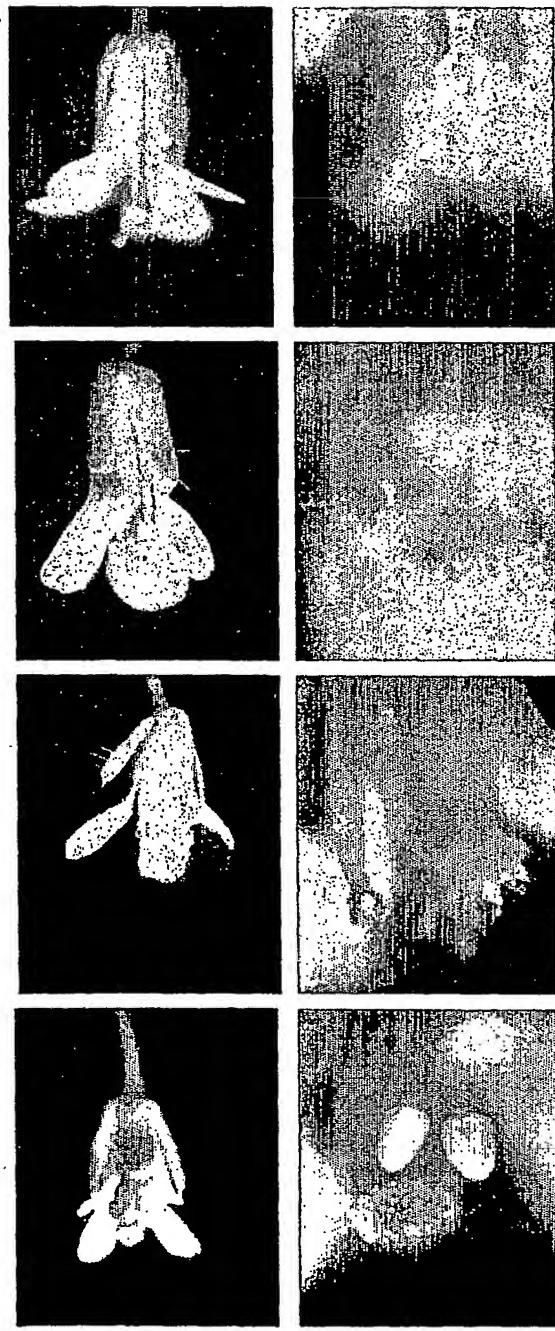


Fig. 36

Male sterile transgenes in *Arabidopsis thaliana*



RKS10S T1-10 no pollen formed	RKS10a T1-11 almost no pollen	pGreen4K normal pollen	ELS 2 157.21S T1-11 T2-2 pollen development aborted
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